us-09-252-691c-\1394) oli.rge

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OM nucleic - nucleic search, using sw model

January 20, 2003, 23:06:19; Search time 2628 Seconds (without alignments) 7408.591 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

OLIGO\_NUC Gapop 60.0 , Gapext 60.0 Scoring table:

20 Word size :

Total number of hits satisfying chosen parameters:

2054640 segs, 14551402878 residues

Searched:

20

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database :

gb\_pat:\* gb\_ph:\* gb\_pl:\*

gb\_ro:\* gb\_sts:\*

gb\_sy:\* gb\_un:\* gb\_vi:\* em\_ba:\*

em\_hum:\* em\_in:\* em\_mu:\* em\_om:\*

em\_or:\*
em\_ov:\*
em\_pat:\*
em\_ph:\*
em\_ph:\*

em\_sts:\*
em\_un:\*
em\_v1:\*
em\_v1:\*
em\_btg\_hum:\*
em\_htg\_luv:\*
em\_htg\_other:\*

em\_htg\_pln:\*
em\_htg\_rod:\*
em\_htg\_mam:\*
em\_htg\_vrt:\*
em\_htg\_vrt:\*

em\_htgo\_hum:\* em\_htgo\_mus:\* em\_htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

|           |                               | 1.                 |                    |                    |                    |                    |                    |                    |                    |                   |                   |                    |                    |                   |                    |                    |                    |                    |                    |                   |                    |  |
|-----------|-------------------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|-------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--|
|           | Description                   | AE000213 Escherich | AE005329 Escherich | D90748 Escherichia | D90749 Escherichia | AC073744 Mus muscu | AP002555 Escherich | AE008754 Salmonell | AL627269 Salmonell | AE013675 Yersinia | AJ414157 Yersinia | AF415022 Chamaebat | AB064593 Escherich | AE013782 Yersinia | U55370 Caenorhabdi | AC106775 Homo sapi | AC128922 Rattus no | AC004021 Human PAC | AC116356 Homo sap1 | AJ414149 Yersinia | AL353689 Human DNA |  |
| SUMMAKIES | αI                            | AE000213           | AE005329           | D90748             | D90749             | AC073744_0         | AP002555           | AE008754           | AL627269           | AE013675          | AJ414157          | AF415022           | AB064593           | AE013782          | U55370             | AC106775           | AC128922           | AC004021           | AC116356           | AJ414149          | AL353689           |  |
|           | В                             | -                  | 1                  | 1                  | ÷                  | 2                  | П                  | П                  | П                  | П                 | П                 | æ                  | П                  | _                 | m                  | 6                  | 7                  | 6                  | 7                  | -                 | σ                  |  |
|           | l<br>Query<br>Match Length DB | 10959              | 11732              | 15007              | 20284              | 110000             | 222605             | 24578              | 254050             | 10393             | 216050            | 884                | 7770               | 10473             | 32403              | 137586             | 152037             | 171370             | 175838             | 193050            | 195829             |  |
| d         | Query<br>Match                | 3.4                | 3.4                | 3.4                | 3.4                | 3.4                | 3.4                | 3.3                | 3.3                | 3.1               | 3.1               | 3.0                | 3.0                | 3.0               | 3.0                | 3.0                | 3.0                | 3.0                | 3.0                | 3.0               | 3.0                |  |
|           | Score                         | 23                 | 23                 | 23                 | 23                 | 23                 | 23                 | 22                 | 22                 | 21                | 21                | 20                 | 20                 | 20                | 20                 | 20                 | 20                 | 20                 | 20                 | 20                | 20                 |  |
|           | Result                        | 0                  | 0                  | 3                  | c<br>4             | c<br>5             | 9<br>0             | c 7                | œ<br>ن             | 6                 | c 10              | 11                 | c 12               | c 13              | 14                 | c 15               | c 16               | 17                 | c 18               | c 19              | c 20               |  |
|           | Res                           | b                  | υ                  | υ                  | υ                  | ပ                  | ပ                  | ပ                  | υ                  |                   | O                 |                    | ပ                  | O                 |                    | υ                  | O                  |                    | υ                  | O                 | υ                  |  |

| AE000213 10959 bp DNA linear BCT 01-DEC-2000 Escherichia coli K12 MG1655 section 103 of 400 of the complete genome. AE000213 U00096 AE000213.1 GI:1787371 | Escherichia coli K12. Escherichia coli K12 Bacteria: Proteobacteria: gamma subdivision; Enterobacteriaceae; Escherichia. 1 (bases I to 10959. 1 (bases I to 10959. 1 (bases I K. Plunkett, G. III, Bloch, C.A., Perna, N.T., Burland, V., Riley, M., Collado-Vides, J., Glasner, J.D., Rode, C.K., Mayhew, G.F., Gregor, J., Davis, N.W., Kirkpatrick, H.A., Goeden, M.A., Rose, D.J., Mau, B. and Shao, Y. | The complete genome sequence of Escherichia coli K-12 Science 277 (5331), 1453-1474 (1997) 97426617 978503 2 (bases 1 to 10959) Blattner,F.R. Direct Submission Submitted (16-JAN-1997) Guy Plunkett III, Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA. Email: ecoli@genetics.wisc.edu Phone: 608-262-2534 Fax: 608-263-7459 | 3 (bases 1 to 10959) Blattner,F.R. Direct Submission Submitted (02-SEP-1997) Guy Plunkett III, Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA. Email: ecoli@genetics.wisc.edu Phone: 608-262-2534 Fax: 608-263-7459 4 (bases 1 to 10959) Plunkett,G. III. Direct Submission Submitted (13-OCT-1998) Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA |
|---|---|---|--|
| RESULT 1 AE000213/C LOCUS DEFINITION ACCESSION VERSION KEYWORDS   | SOURCE<br>ORGANISM<br>REFERENCE<br>AUTHORS (  | TITLE<br>JOURNAL<br>MEDLINE<br>PUBMED<br>REFERENCE<br>AUTHORS<br>TITLE<br>JOURNAL   | REFERENCE<br>AUTHORS<br>TITLE<br>JOURNAL<br>AUTHORS<br>TITLE<br>JOURNAL  |

COMMENT

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promoter
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This sequence was determined by the E. coli Genome Project at the University of Misconsin-Madison (Frederick R. Blattner, director). Supported by NIH grants HG00301 and HG01428 (from the Human Genome Project and NCHGR). The entire sequence was independently determined from E. coli Kl2 strain MG1655. Predicted open reading frames were determined using GeneMark software, Kindly supplied by Mark Borodovsky, Georgia Institute of Technology, Atlanta, GA, 30332 [e-mail: mark@amber.gatech.edu]. Open reading frames that have been correlated with genetic loci are being annotated with CG Site Nos., unique ID nos. for the genes in the E. coli Genetic Stock Center (GGSC) database at Yale University, kindly supplied by Mary Berlyn. A public version of the database is accessible (http://cgsc.blology.yale.edu). Annotation of the genome is an ongoing task whose goal is to make the genome sequence more useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Riley; added promoters, protein binding sites, and repeated sequences described in reference 1. The unique numeric identifiers beginning with a lowercase 'b' assigned to each gene (protein or RNA-encoding) are now designated as gene synonyms instead of labels. This should allow them to be searched for in Entrez as gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MDKLLERFLNYVSLDTQSKAGVRQVPSTEGQWKLLHLLKEQLEE
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YIIRDFDRKQFEARKRKMMEIAKKVGKGLHPDCYIELVIEDSYNMREKVVEHPHILD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                by correlating it with other data. Comments to the authors are appreciated updated information will be available at the E. coli Genome Project's World Wide Web Site (http://www.genetics.wisc.edu). *** The E. coli K12 sequence and its annotations are periodically updated; this is version M54. No sequence changes. Annotation updates: updated gene identifications and products; all new functional assignments courtesy of Monica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /EC_number="3.4.11.-"
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/function="putative enzyme; Not classified"
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PEPT_ECOLISW: P29745; 93 pet identical to 407 residues of
409 aa PEPT_SALTY SW: P26311"

    .40
    /note="factor Sigma70; predicted +1 start at 1184959"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119. .136
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155. .1381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(1430, .2560)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="b1128"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             155. .1381
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HSIKTPLAVLOSTLRSIRSEKMSVSDAEPVMLEQISRISQQIGYYLHRASMRGGTLLS
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EITEQYEGKIYAGESMLGGARWEGTREFFENTEDFES
COMPIEMENT (4087. .4758)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KVAEIPELHAVSEFIHFACTSEDINNISHALMIKTARDEVILPYWRQLIDGIKDLAVO
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complement(2583. 2513)
Anote-Tactor Sigma70; predicted +1 start at
complement(2627. .4087)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /transl_table=11
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/note="b1131"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="b1130"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="purB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="phop"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="pho0"
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MVDELK"
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MRRYGIEKPYEKLKELTRGKRVDAEGMKQFIDGLALPEEEKARLKAMTPANYIGRAIT
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DMNPSSTLAVFGGSEANLRVGLETLLGVLNASSRQGLNAELTRYTLSLMVLERKLSSA
                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BCT 21-MAR-2003
3, section 153
                                                                                                                                        /function="orf; Unknown"
/note="f213; 99 pct identical to YCFC_ECOLI SW: P25746"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Perna, N.T., Punkett, G. III, Burland, V., Mau, B., Glasner, J. D., Rose, D. J., Mayhew, G. F., Evans, P. S., Gregor, J., Kirkpatrick, H. A., Postai, G., Hackett, J., Klink, S., Boutin, A., Shao, Y., Miller, L., Grotbeck, E. J., Davis, N.W., Lim, A., Dimalanta, E., Potamousis, K., Apodaca, J., Anantharaman, T. S., Lin, J., Yen, G., Schwartz, D. C., Welch, R. A. and Blattner, F. R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 11732)
Pernah. NT., Plunkett,G. III, Burland,V., Mau,B., Glasner,J.D.,
Rose,D.J., Mayhew,G.F., Evans,P.S., Gregor,J., Kirkpatrick,H.A.,
Posfai,G., Hackett,J., Klink,S., Boutin,A., Shao,Y., Miller,L.,
Grotbeck,E.J., Davis,N.W., Lim,A., Dimalanta,E., Potemnousis,K.,
Apodaca,J., Anantharaman,T.S., Lin,J., Yen,G., Schwartz,D.C.,
Welch,R.A., and Blattner,F.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7
                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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/function="enzyme; Nucleotide biosynthesis: Purine
ribonucleotide biosynthesis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         University
                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                     Score 23; DB 1; Length 10959;
Pred. No. 0.19;
7. Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AE005329 11732 bp DNA linear Escherichia coli 0157:H7 EDL933 genome, contig 1 of of 155.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Escherichia coli 0157:H7 EDL933'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (22-ocr-2000) Laboratory of Genetics, Ur
Wisconsin, 445 Henry Mall, Madison, WI 53706, USA
Location/Qualifiers
1. 11732
                                                                                                                                                                                                                                          /product="orf, hypothetical protein"
/protein_id="AAC74216.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="enterohemorrhagic"
complement(115. .1485)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 409 (6819), 529-533 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /serotype="0157:H7"
/db_xref="taxon:155864"
                                                                                               complement(6301. .6942)
/gene="ycfc"
                                        complement(6301. .6942)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Escherichia coli 0157:H7 EDL933
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9136 CTGTTCAATAAACCCTACGATGT -9114
                                                                                                                                                                                                                     /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                             133 CTGTTCAATAAACCCTACGATGT 155
                                                                                                                                                                                                                                                                                                                                                              3.4%; Sur.
100.0%; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /strain="EDL933'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GI:12514784
                                                                                    /note="b1132"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Z1860"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 11732)
                                                                    ycfC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="purB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AE005329 AE005174
                                                                    /gene="
                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 23; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AE005329.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
JOURNAL
                                             gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene
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residues 1 to 383 of 383 from Escherichia coli K-12 Strain
MG1655: B1133"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /function="orf; Unknown function"
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DMNPSSTLAVPGGSRANLRVGLETLIGVLNASSRQGINAEITRYTLSLAVLRKLSSA
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PQVQAKVRATLLAGIRAAVLAHQVGGGRLQLAFSRNRLTTQAKQILAHLTPEL"
complement(2166 . 3317)
to 456 of 456 are 99.78 pct identical to of 456 from Escherichia coli K-12 Strain
                                                                                                                                                                                                                                                                      /translation="MELSSLTAVSPVDGRYGDKVSALRGIFSEYGLLKFRVQVEVRWL
KOLAHAAIKEVPARADAIGYLDALYANFSEEDAARIKTIERTINIDYKAVEYFLKE
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YRDIPLLSRTHGQPATDSTIGKEMANVAYRWERQYRQLINOVEILGKINGAGVGRYNAHI
AAYPEVDWHQFSEEFVTSLGIQWNPYTTQIEPHDYIAELFDCVARFNTILIDFDRDVW
                                                                                                                                                                                                                                                                                                                                                                                                                                          GYTALNHFRÖKTTAGEIGSSTWPHKVNPIDFENSEGNLGLSNAVLQHLASKLPVSRWQ
RDLTDSTVLRNLGVGIGYALIAYQSTLKGVSKLEVNRDHLLDELDHNWEVLAEPIQTV
MRRYGIEKPYEKLKELTRGKRVDAEGMKQFIDGLALPEEEKARLKAMTPANYIGRAIT
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YQVEGLFMKNWEEDDGEEYCTAAADLADAQAVCDKLGIELHTVNFAAEYWDNVFELFL
AEYKAGRTPNPDILCNKEIKFKAFLEFAAEDLGADYIATGHYVRRADVDGKSRLLRGL
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RFREELGEATKLDAQGHEHPRIJAGOLGENGGLAWTHIGQRKGLGIGGTREGTEEFWYV

VDKDVENNILIVAQGHEHPRIJAGOLHWYDREPFTGTWRCTYKTRYRQTDIPC

TVKALDDDRIEVIFDEPVAAVTPGQSAVFYNGEVCLGGGIIEORLEPI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MFKPHVTvACVVHAEGKFLVVEETINGKALWNOPAGHLEADETL
VEAARELWEETGSAQPHETRWHOWIAPDKTPFLRRLFATELEQ.CCPTQPHDSDID
CCRWVSAETLLQASLLSPLVAESIRCYQSGQRYPLEMIGDFNWPFTKGVI"
complement(3797. .4420)
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/function="putative enzyme; Not classified"
/note="Residues 1 to 153 of 153 are 100.00 pct identical
to residues 1 to 153 of 153 from Escherichia coli K-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="putative phosphohydrolase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /transl_table=11
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                                                                                                                                                                                                       /protein_id="AAG55957.1"
/db_xref="G1:12514785"
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/gene="z1863"
complement(3326. .3787)
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/note="Residues 1
residues 1 to 456
MG1655: B1131"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="ycfC"
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Oshima, T., Aiba, H., Baba, T., Fujita, K., Hayashi, K., Honjo, A., Oshima, T., Aiba, H., Isba, T., Itoh, T., Kajihara, M., Kanai, K., Rashimoto, K., Kimura, S., Kitagawa, M., Makino, K., Masuda, S., Miki, T., Micobuchi, K., Mori, H., Motomura, K., Nakamura, Y., Nashimoto, H., Nishio, Y., Saito, N., Sampei, C., Sekil, Y., Tagami, H., Takemoto, K., Wada, C., Yamamoto, Y., Yano, M. and Horiuchi, T. A. 718-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage map DNA Res. 3 (3), 137-155
                                                                                                                                                                        /translation="mSRLITLRDWAKEEFGDLAPSERVLKKYAQGKMMAPPAIKVGRY
WMIDRNSRFVGTLAEPQLPINANPKLQRIIADGC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Aiba, H., Baba, T., Fujita, K., Hayashi, K., Honjo, A., Horiuchi, T., Ikemoto, K., Inada, T., Isono, S., Itoh, T., Kanai, K., Kasai, H., Kashimoto, K., Kim, S., Kim, S., Kimaya, M., Kitakawa, M., Makino, K., Masuda, S., Miki, T., Mizobuchi, K., Mori, H., Moroura, K., Nakamura, Y., Nashimoto, H., Nishio, Y., Oshima, T., Yamamoto, Y. and Yano, M. Tayami, H., Takemoto, K., Mada, C., Yamamoto, Y. and Yano, M. The systematic sequencing of the Escherichia coli genome in Japan Unpublished

3 (bass 1 to 15007)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 D90748.1 GI:1651553
Complete and shotgun sequencing; potB; potA; pepT; phoQ; phoP; purB; ycfC; ycfB; icdA; icdA; icdE; lit.
Escherichia coli(strain:K12) DNA, clone:Kohara clone #239.
Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (29-JUL-1996) Hirotada Mori, NARA Institute of Scie
and Technology, Res. & Edu. Center for Genetic Info.; 8916-5
Takayama, Ikoma, Nara 630-01, Japan
(E-mall:hmori@qtc.alst-nara.ac.jp, Tel:81-7437-2-5660,
Exx:81-7437-2-5660,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alba, H. Japan E. coli genome DNA sequencing group
Members: (1995.4 - 1996.3)
Alba, H., Baba, T., Fujita, K., Hayashi, K., Honjo, A.,
Horiuchi, T., Ikemeto, K., Inada, T., Isono, K., Isono, S.,
Itoh, T., Kanai, K., Kasai, H., Kashimoto, K., Kim, S.,
Kimura, S., Kitagawa, M., Kitakawa, M., Makino, K.,
Masuda, S., Miki, T., Mizobuchi, K., Mori, H., Motomura, K.,
Nakamura, Y., Nashimoto, H., Nishio, Y., Oshima, T., Saito, N.,
Sampei, G., Seki, Y., Tagami, H., Takemoto, K., Wada, C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15007 bp DNA linear Escherichia coli genomic DNA. (25.6 - 25.9 min). D90748 ABO01340
                                                                                                                                                                                                                                                                                                                                                   0; Indels
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                                                                                                                                                                                                                                                                                         DB 1;
0.19;
                                                                                                                                                                                                                                                                                                         100.0%; Preu. ...
                                                                                                                                                                                                                                                                                      Score 23;
Pred. No.
[Bacteriophage 21]"
                                                                                                                                                                                                                                                                                                                                                                                                                                            4324 CTGTTCAATAAACCCTACGATGT 4302
                                                                                                                                                                                                                                                                                                                                                                                                              133 CIGITCAATAAACCCTACGAIGT 155
                                                                                                                                                                                                                                  7458. .8201
                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                   23;
                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                           Local
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TITLE
JOURNAL
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JOURNAL
REFERENCE
                                                                                                                                                                                                                                                                                                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
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D90748/c
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                                                                                                                                                                                                                                                                                                                                                                                                              δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                          complement(3797. .4420)
/gene="ymfC"
/function="orf; Unknown function"
/funce="kesidues 1 to 207 of 207 are 99.03 pct identical to residues 1 to 207 of 207 from Escherichia coli K-12 Strain MG1655: B1135"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGIEWRADSADAEKVIKFLREEMGVKKIRFPEHCGIGIKPCSEEGTKRLVRAAIEYAI
ANDROSYLVHGKUINKFFTEAFKUMGVELAREEFGGELIOGOFWLKWINPWIGKEIV
IKDVIADAFLOGILLERAEYDVIACHNILNGSPEGGELIOGOFWLKWINPWIGKEIV
EEATHGTAPKYAGODKVNPGSIILSAEMMLRHMGWTEAADLIVKGMEGAINAKTVTYD
FERLMEGARLLKCSEFGDAIIKNM"
5791. .>11732
/note="O-island #52; Region of the EDL933 chromosome not
complement(5986. .7128)
/gene="21866"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="21866"
/function="putative enzyme; Integration, recombination
/function="putative enzyme; Integration, recombination
/note="Residues 1 to 380 of 380 are 98.42 pct identical to
residues 1 to 380 of 380 from GenPept 118 :
gi[215450[gb]AAA32336.1] (M61865) integrase [Bacterlophage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /function="enzyme; Energy metabolism, carbon: TCA cycle" //note="Residues 1 to 416 of 416 are 99.27 pct identical to residues 1 to 416 of 416 from Escherichia coli K-12 Strain MG1655: B1136"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product-"isocitrate dehydrogenase, specific for NADP+"
/protein id-"AAG55962.1"
/bc.xref-"GI:12514790"
//translation-"REXVVVPAQGKKITLONGKLNVPENPIIPYIEGDGIGVDVTPA
MLKVVDAAVERAYKGERKISHMEIYYGEKSYQVYGQDVWLPAATLIDIREYRYAIKGP
LITTPYGGGIRSLNVALRQELDLYICLRPVRYYQGTPSPVKHPELTDMVIFRENSEDIY
                                                                                                                                                                                                                                                                                                                                                                         /translation="MOKTSFRNHQVKRFSSORSTRRKPENQPTRVILFNKPYDVLPQF
TDSGRKTTEEIPVGGYPAAGRLDRDSEGILVTUNGALGARITQPGKRTGKIYYO
VEGIPTQDALEALRMGYTLANGGPTLPAGAEIVDEPAMLWPRNPIRERKSIPTSWLKI
TLYBGRNRQVRRWTAHVGFPTLELIRYAMGDYSLDNIANGEMRRATE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="maasprshkisipnlyckldkrtckvywqykhplsgrfhslgtd
Enbakqvateantilaeqrtrqilsynerlermkgrrsditytewldkynsiqedrlo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HNELRPNSYRQKGKPIRLFREHCGMOHLKDITALDIAEIIDAVKAEGHNRMAÕVVRMV
LIDVFKEAQHAGHVPPGFNPAQATKQPRNRVNRQRLSLPEWQAIFDSVSRRQPYLKCG
MLALVTGORLSDICNLKFSDIWDDMLHITQEKTGSKLAIPLNLKCDALNITLREVIS
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RSLSERLYREQGLDTQKLLGHKSRKMTDRYNDDRGKDWIIVDIKTA"
complement(7118. .7354)
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//note="Residues 1 to 78 of 78 are 98.71 pct identical to residues 1 to 78 of 78 from GenPept 118 : 91/215449|gb|AAA32335.1| (M61865) excisionase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /function="putative enzyme; Integration, recombination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
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/db_xref="GI:12514791"
                                                                                                                                                                                                                                                                                   /product="orf, hypothetical protein"
/protein_id="AAG55961.1"
/db_xref="G1:12514789"
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                                                                                                                                                                                                                               /codon_start=1
/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note-"Z1865"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4622. .5872
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/gene="icdA"
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Science

BCT 07-FEB-1999

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Gaps

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VNYYPATSRMPKLTIVVVDTIPVELKSSYMVWSWFIYVLSANLLLYIPLLUPLWVAAWWSL
RPIRALKEYRELEBHNRELLNPSTRELTSLYRNLAKSERSDKYKTTUTDLT
HSLKTPLAVLGSTLRSLRSERKWSVSDAEPWALEQ1SRISQOIGYYLHRASMRGGTLLS
RELHPVAPLLDNLTSALNKVYQRKGVNISLDISPEISFVGEQNDFVEVWGNVLDNACK
YCLEFFYETSRAPPORTIVIVEDDOGFOFFERSKRSKNEN"
                                                           Y II RDFDRKQFEARKRKMME IAKKVGKGLHPDCY I ELV I EDSYYNMREKVVEHPH I LD
I AQQAMRDCD I EPELKP I RGGTDGAQLSFMGLPCPN LFTGGYNYHGKHEFVTLEGMEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MEYQLTLNWPDFLERHWQRRPVVLKRGFNNFIDPISPDELAGLA MESEVDSRVJCSHQVSKHWHEPTRALMPFRE LIPDRRIDDLAISFSVPGGGVGPHLDQYDVFIJGGTGRRWRWCGKLQMKQHCPHPDLL QVDPFBAIIDEAPPTIGGTGRRWRWCGKLQMKQHCPHPDLL QVDPFBAIIDEELEPGDILYIPPGFPHEGYALENAMNYSVGFRAPNTRELISGFADYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LQRELGGNYYSDPDVPPRAHPADVLPQEMDKLREMMLELINQPEHFKQWFGEFISQSR
HELDIAPPEPPYQPDEIYDALKQGEVLVRLGGLRVLRIGDDVYANGEKIDSPHRPALD
ALASNIALTAENFGDALEDPSFLAMLAALVNSGYWFFEG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MRVLVVEDNALLRHHLKVQIQDAGHQVDDAEDAKEADYYLNEHI
PDBAIVDLGEDEDGLELIRRWRSNDYSLPILTATARESWQDKVEVLSAGADDYYTKP
FHIEEVWARWQALMRNSGLASQVISLPPFQVDLSRRELSINDEVIKLTAFEYTIMET
LIRNNGKVVSKDSLMLQLYPDAELRESHTIDVLMGRLRKKIQAQYPQEVITTVRGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MELSELTANSPVDGRYGDKVSALRGIFSEYGLLKFRVQVEVRML
OKLAMHAAIKEVPAFRADAIGYLDAIVASFSEEDAARIKTIERTINDVKAVEYFLKE
VAREIPELHAVSEFIHFACTSEDINNISHALMKTARDEVILPYWRQLIDGIKDLAV
YRDIPLISRTHGQPATPSTIGKEMANVAYRMERQYRQLINQVEILGKINGAGVGRYNAHI
AAYPEVDWHQFSEEFVTSLGIGWNPYTTQIEPHDYIAELFDCVARFNTILIDFDRDVW
      PHGDIRVAFTPDEEVGKGAKHFDVDAFDARWAYTVDGGGVGELEFENFNAASVNIKIV
                                     GNNVHPGTAKGVMVNALSLAARIHAEVPADESPEMTEGYEGFYHLASMKGTVERADMH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="Transcriptional regulatory protein PhoP."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="ORF_ID:0240#1
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                                                                                                                                                                                                                                                                     /note="ORF_ID:0239#3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="ORF_ID:0239#4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EITEQYEGKIVAGESMLGGARMEVIFGRQHSAPKDE'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(6010. .6681)
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                                                                                                                          AVQVIVRIAELTAQRK"
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                                                                                                                                                                                                                                               /gene="pho0"
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LLDPDAFEVLHSLMMALIATLACULGYPPFWTAKLPHKNPLLLFLLLFLIVPFWTN
SLIRIYGLKIFVLKFVLNEFLLWLGVIDTPRRIPPSAVIIGLVYILPFWYMPLY
SSIEKLDKPLLERARRDLGASKLQFFIRIIIPLTMPGIIAGCLLVWLPAMGLFYSDLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MGQSKKLNKQPSSLSPLVQLAGIRKCFDGKEVIPQLDITINNGE"
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HMTVFENVAFGLRMQKTPAAEITPRVMEALRWVQLETFAQRKPHQLSGGQQQRVAIAR
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IALGIGDEVLSPVMFPVLHQLLGQTLITTDGKTLLGADDKAGIAEIMTALAVLQQKKI
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VYMROGRIGDOGTPRETYEBFKNLFYAKGFIGETNMFNATVIERLDEORYRANVEGREC
NIYVNRAVERGGKLHTYLLRPEDLRVEEINDDHAEGLIGYVRERNYKGMTLESVVELE
NGKMVMVSEFFNEDDPFDHSLLOKMAINWVESWEVVLADEEBHK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /transl_table=11
/product="Spermidine/putrescine transport system permease
protein PotB."
                                                                                        of Basic Biology, Okazaki, 444, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="Peptidase T (EC 3.4.11.-) (aminotripeptidase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /un__iter__carrows.
/map="25.5 min"
/clone="Kohara clone #239"
/note="Nucleotide position 1185468-1200474 from the
initiation site of ThrA (0 min.).-This clone is from
Kohara lambda miniset library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="Spermidine/putrescine transport protein A"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="ORF_ID:0238#14
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                                                                                                                                       Information operator:
Name: Hirotada Mori
Address: NARA Institute of Science and Technology,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="potA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism-"Escherichia coli"
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/db_xref-"taxon:562"
                                                                                                                                                                                                                                                                                                                        The Japan E. coli genome database http:bsw3.aist-nara.ac.jp.
Location/Qualiflers
                                                                                                                                                                                                                                                                  E-mail: hmori@gtc.aist-nara.ac.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="BAA35947.1"
/db_xref="GI:1651554"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="potA"
complement(692. .1828)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="potB"
complement(<1. .678)
                                                                                                                                                                                                                                         Ikoma, 630-01, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="ORF_ID:0239#2
                                                                                     Address: National Institute
E-mail: kishori@nibb.ac.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(1. .678)
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Yamamoto, Y. and Yano, M.
                                                        Name: Takashi Horiuchi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
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/gene="pepT"
2078. .3304
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Oshima, T., Aiba, H., Baba, T., Fujita, K., Hayashi, K., Honjo, A., Ikemoto, K., Inada, T., Itoh, T., Kajihara, M., Kanai, K., Kashimoto, K., Kinara, S., Kitagawa, M., Makino, K., Masuda, S., Miki, T., Mizobuchi, K., Mori, H., Motomura, K., Nakamura, Y., Nashimoto, H., Mishio, Y., Saito, N., Sampel, G., Seki, Y., Tagami, H., Takemoto, K., Wada, C., Yamamoto, Y., Yano, M. and Horluchi, T. A. 18 kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage map DNA Res. 3 (3), 137-155 (1996)
GYIALNHFKQKTIAGEIGSSTMPHKVNPIDFENSEGNLGLSNAVLQHLASKLPVSRWQ
RDLTDSTVLRNLGVGIGYALIAYQSTLKGVSKLEVNRDHLLDELDHNWEVLAEPIQTV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Address: National Institute of Basic Biology, Okazaki, 444, Japan
E-mail: kishori@nibb.ac.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (29-JUL-1996) Hirotada Mori, NARA Institute of Science and Technology, Res. & Edu. Center for Genetic Info.; 8916-5 trayayama. Ikoma. Nara 630-01, Japan (E-mail:hmori@qtc.aist-nara.ac.jp, Tel:81-7437-2-5660,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                 Escherichia coli genomic DNA. (25.7 - 26.1 min).
D90749 AB001340
D90749 1 G1:165:162
Complete and shotgun sequencing; phoQ; phoP; purB; ycfC; ycfB; hcdA; lcd; lcdE; lit; lnt; xis; ycfE; ycfE; pin; ycfA.
Escherichia coli(strain:K12) DNA, clone:Kohara clone #240.
                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The Japan E.coli genome DNA sequencing group
Members: (1995.4 - 1996.3)
Alba.H., Baba.T., Fujita, K., Hayashi, K., Honjo, A.,
Horluchi, T., Ikemcto, K., Inada.T., Isono, K., Isono, K.,
Itoh.T., Kanal, K., Kasai, H., Kashimoto, K., Kim, S.,
Kimura, S., Kitagawa, M., Kitakawa, M., Makino, K.,
Masuda, S., Miki, T., Mizobuchi, K., Mori, H., Motomura, K.,
Nakamura, Y., Mashimoto, H., Nishio, Y., Oshima, T., Saito, N.
Sampei, G., Seki, Y., Tagami, H., Takemoto, K., Wada, C.,
Hoadad, M.,
                                                                                                                                               ·,
                                                                                      Length 15007;
                                                                                                                                                                                                                                                                                                                                                                                             bp DNA linear (25.7 - 26.1 min).
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                                                                                      DB 1;
0.19;
                                                                                   3.4%; Score 23; DB 100.0%; Pred. No. 0.1
Live 0; Mismatches
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                                                                                                                                                                                             CTGTTCAATAAACCCTACGATGT 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name: Takashi Horiuchi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 20284)
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Name: Hirotada Mori
                                                                                                                                         23; Conservative
                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (sites)
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VERSION
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AUTHORS
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JOURNAL
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JOURNAL
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SOURCE

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PDIAIVDLGLPDEDGLSLIRRWRSNDVSLPILVLTARESWQDKVEVLSAGADDYVTKP
FHIEEVWARWQALMRRNSGLASQVISLPPFQVDLSRRELSINDEVIKLTAFEYTIMET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="Adenylosuccinate lyase (EC 4.3.2.2)"
/profuein_id="BAA55962.1"
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KVAEIPELHANSEFTHFACTSEDINNLSHALMLKTARDEVILPYWRQLIDGFKDLAV
FRIPTLIGPRIGOPATPSTIGKEMANVAYRMERQYRQLNQVELLGKKINGAVGRYNAHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MKKLLKLFFPLSLRVRFLLATAAVVLVLSLAYGMVALIGYSVSF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAYPEVDWHQFSEEFVTSLGIQWNPYTTQIEPHDYIÄELFDCVARFNTILIDFDRDWW
SYALAHWFROKYIAGEIGSSYMPHKVNPIDFENBSGNIGLSBANJQHLASKLPVSRWO
RDLTDSTVLRALGYGIGYALIAYQSTLKGVSKLEVNRDHLLDELDHWWPVLAEPIQTV
MRRYGIEKPYEKLKELFRGKRVDAEGWKQFIDGLALPBEEKARLKAMTPANYIGRAIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LIRNNGKVVSKDSLMLQLYPDAELRESHTIDVLMGRLRKKIQAQYPQEVITTVRGQGY
                                                                                                                                                                                                                                                                                               /map="25.7-26.1 min"
/clone="Kohara clone #240"
/clone="Nolacotide position 1191151-1211434 from the initiation site of ThrA (0 min.).-This clone is from Kohara lambda miniset library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
/transl_table=11
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/db_xref="G1:1651563"
Address: NARA Institute of Science and Technology, Ikoma, 630-01, Japan
E-mail: hmori@gtc.aist-nara.ac.jp
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                                                                                                          The Japan E. coli genome database http:bsw3.aist-nara.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(1167. .2537)
/gene="purB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(2541. .3182)
/gene="ycfC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(1167. .2537)
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                                                                                                                                                                                                                     /organism="Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(327. .998)
/gene="phop"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(327. .998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(<1. .327)
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                                                                                                                                                                                                                                                                        /db_xref="taxon:562"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="phoo"
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5376 CIGITCAAIAAACCCIACGAIGI 5354

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Consensus quality: 310234 bases at least Q40
Consensus quality: 387412 bases at least Q30
Consensus quality: 406374 bases at least Q30
Consensus quality: 406374 bases at least Q30
Consensus quality: 406374 bases at least Q30
Estimated insert size: 47339; sum-of-contigs estimation
Estimated insert size: 47339; sum-of-contigs estimation
Quality coverage: 5.77 in Q20 bases; pulse field gel estimation

* NOTE: This is a "working draft' sequence. It currently

* consists of 196 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
                                                                                                                                                                                                                                                                                                                                                           A\overline{C}073744 466859 bp DNA linear HTG 12-JUL-2000 Mus musculus clone RP23-288A3, WORKING DRAFT SEQUENCE, 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (29-JUN-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                LOCUS AC073744 Accession AC073744
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1252: gap of unknown length
2396: contig of 1144 bp in length
2496: gap of unknown length
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Center: Joint Genome Institute
Center Code: JGI
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PQVQARVRATLLAGIRAAVLWHQVGGGRLQLHFSRNRLITQAKQILAHLIPEL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MFKPHVTVACVVHAEGKFLVVEETINGKALWNOPAGHLEADETL
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complement(49. .5502)
/note="ORF_LD:0240#6
similar to PIR Accession Number 164156"
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NKPYDVLPQFTDEAGRKTLKEFIPVQGVYAAGRLDRDSEGLLVLTNNGALQARLTQPG
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GEEYCTAAADLADAQAVCDKLGIELHTVNFAAEYWDNVFELFLAEYKAGRTPNPDILC
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GKIITVDGDEIGEHQGLMYHTLGQRKGLGIGGTKEGTEEPWYVVDKDVDNNILVVAQG
HEHPRLMSVGLIAQQLHWVDREPFTGTWRCTVKTRYRQTDIPCTVKALDDDRIEVIFD
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KSIPTSWLKITLYEGRNRQVRRMTAHVGFPTLRLIRYAMGDYSLDNLANGEWREVTD"
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/product="Hypothetical protein in purB 5'region (orf-15)
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similar to SwissProt Accession Number P25745"
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/protein_id="BAA35965.1"
/db_xref="G1:4062716"
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similar to PIR Accession Number S64074"
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complement(4378. .4839)
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complement(3218. .4324)
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5674. .6924
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Query Match 3.4%; Scc Best Local Similarity 100.0%; Pr Matches 23; Conservative 0;

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RESULT 6 AP002555/c

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NSLRLVAANSYTSVAFPAISTGVYGYPRAAABIAVKTVSEFITRHALPEQVYFVCYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="mnpvPaQREYFLDSIRAWLMLGIPFHISLIYSSHTWHVNSAEP
SLMLTLENDETHSFRAQVFYISGYESYMLENEYPERKVKVRYGERQIDMLTAPLL
TLPQFIMLQYVKQRESSWPGLSIZYNKYNTLAMELISHLWFLLVLVVWTTLCVWIFKRI
RNNLENSDKTNKKFSWVKLSVIFLCLGIGYAVIRRTIFIVYPPILSNGTFNFIVWQTL
FYLPFRIIGALAFIFPHLKALFTTPRSKCTLAAALAFVAXLLANGRYGSGDAWYETES
VITWYLGIMYNVVYSFGHRLLNFQSARVTYFVNASLFIYLVHHPLTLFFGSDAWYETES
TSNWLGFLCGLIFVVGIAIILYEIHLRIPLLKFFISGKPVVKRENDKAPARR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KFVVMPGRDTVVDVQSKIYLRDKVGKLGVAPLTSMFLFGPNQPSPANNYRPELHDSNG
LLSTHAGNGEWIWRPLNNPKHLAVSSFSMENPOGFGLLQRGRDFSRFEDLJDBKYDLRPS
AWYTPKGEWGKGSVELVEITNDETNDNIVAVWPTPQLPEPGKEMNFKYTITESRDED
KLIARPDNARVQQTRSKTGDVKGSNILRQPDGTIAFVVDFTGAEMKLPEDTPYTAQTS
IGDNGEIVESTVRYNPVTKGWRLVMRVKVKDAKKTTEMRAALVNADQTLSETWSYQLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NTPGLDDILRLLDSHPRIEVRLFNPFSFRLLRPLGY ITDFSRLNRMHNKSFTVDGVV
TLVGGRNIGDAYFGAGEEPLFSDLDVMAIGPVVEDVADDFARYWYCKSVSPLQQVLDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PEGEMADRIELPASWHNDAMTHRYLRKMESSPFINHLVDGTLPLIWAKTRLLSDDPAK
GEGKAKRHSLLPQRLFDIMGSPSERIDIISSYFVPTRAGVAQLLRWYRKGVKIAILTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SLAANDVAVVHAGYARWRKKLLRYGVELYELKPTREQSSTLHDRGITGNSGASLHAKT
FSIDGKTVFIGSFNFDPRSTLLNTEMGFVIESETLAQLIDKRFIQSQYDAAWQLRLDR
WGRINWVDRHAKKEIVLKKEPATSFWKRVMVRLASILPVEWLL"
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SNLPSVFRDMKYADYQQIQFNHDKAYWNNLKTPFKLEFYHQGMYFDTPVKINEVTATA
VKRIKXSPDYFTFGDVQHDKDTVKDLGFAGFKVLYPINSKDKNDEIVSMLGASYFRVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MMKKTPTSTKDSLPNKEMNDLPRLASAVLPLCSQHPGQCGLFPL
EKSLDAFAARYRLAEMSEHTLDVQYYIWQDDMSGRLLFSALLAAAKRGVRVRLLLDDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAGOVYGLSARGLAIDTALPSGEEFPRFKEFWIERPKPTDKRLTIYALLDSPRATGAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /_____similar to MDOC_ECOLI gil3025226splP75920 percent identity 99 in 385 aa (Conserved in E.coli K-12)" /codon_start=1
                                                                                                                                                                                                                                                                                                                                             /note="similar to YMDC_ECOLI gi|1787284 percent identity 99 in 493 aa (Conserved in E.coli K-12)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="similar to MDOG_ECOLI gil1787286 percent identity 99 in 511 aa (Conserved in E.coli K-12)"
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/protein_id-"BAB34849.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="glucans biosynthesis protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="putative synthase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                      /evidence=not_experimental
/transl_table=11
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/transl_table=11
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/transl_table=11
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/gene="ECs1426"
3588. .5123
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549. .2030
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/gene="ECs1426"
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5086. .7659
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                                                                                                                                                                                                                                                                                                                                                                                                      Sasakawa,C. and Shinagawa,H.
Complete nucleotide sequence of the prophage VT2-Sakai carrying the verotoxin 2 genes of the enterohemorrhagic Escherichia coli 0157:H7 derived from the Sakai outbreak Genes Genet. Syst. 74 (5), 227-239 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complete nucleotide sequence of the prophage VTI-Sakai carrying the Shiga toxin I genes of the enterchemorrhagic Escherichia coli 0157.H7 strain derived from the Sakai outbreak Gene 258 (1-2), 127-139 (2000)
222605 bp DNA linear BCT 07-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (26-JUN-2000) Ken Kurokawa, Osaka University, Genome Information Research Center; 3-1, Yamadaoka, Suita, Osaka 565-0871, Japan (E-mail:ken@gen-info.osaka-u.ac.jp, URL.http://www.gen.info.osaka-u.ac.jp/, Tel:81-6-6879-8365, Fax:81-6-6879-2047)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ohnishi,M., Murata,T., Nakayama,K., Kuhara,S., Hattori,M.,
Kurokawa,K., Yasunaga,T., Yokoyama,K., Makino,K., Shinagawa,H. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="similar to B1045_ECOLI gi|1787283 percent identity 100 in 177 aa (Conserved in E.coli K-12)" /codon_start=1 /evidence=not_experimental
                                                                                                                                        Escherichia coli O157:H7 (strain:O157:H7, sub_strain:RIMD 0509952)
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Ohnishi, M., Kurokawa, K., Makino, K., Yasunaga, T., Shinagawa, H. and
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                                                                                                                                                                                                                                  Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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Yutsudo,C.H., Kurokawa,K., Ishii,K., Hattori,M., Abe,H., Iida,T.
Yamamoto,K., Hayashi,T., Yasunaga,T., Honda,T., Sasakawa,C. and
                                                                                                                                                                                                                                                                                                         Makino,K., Yokoyama,K., Kubota,Y., Yutsudo,C.H., Kimura,S.,
Kurokawa,K., Ishii,K., Hattori,M., Tatsuno,I., Abe,H., Iida,T.,
Yamamoto,K., Ohnishi,M., Hayashi,T., Yasunaga,T., Honda,T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yokoyama, K., Han, C.-G., Ohtsubo, E., Nakayama, K., Murata, T., Tanaka, M., Tobe, T., Iida, T., Takami, H., Honda, T., Sasakawa, C., Ogaswara, M., Yasunaga, T., Kuhara, S., Shiba, T., Hattori, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12 DNA Res. 8 (1), 11-22 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ., Makino, K., Ohnishi, M., Kurokawa, K., Ishii, K.
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                                                     AP002555 BA000007
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AUTHORS
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Locus
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1 (bases 1 to 24578)
McClelland, M., Sanderson, K.E., Spieth, J., Clifton, S.W.,
Latreille, P., Courtney, L., Porwollik, S., All, J., Dante, M., Du, F.,
Hou, S., Layman, D., Leoard, S., Nguyen, C., Scott, K., Holmes, A.,
Grewal, N., Mulvaney, E., Ryan, E., Sun, H., Florea, L., Miller, W.,
Stoneking, T., Nhan, M., Waterston, R. and Wilson, R.K.
Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistries or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one ml3 subclone.

Location_Qualifiers
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/db_xref="G1:16419751"
/translation="MELSSLTAVSPVDGRYGDKVSALRGIFSEYGLLKFRVQVEVRWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GYTALNHFKOKTTAGEIGSSTWPHKVNPIDFENSEGNLGLSNAVLHHLANKLPYSRWO
RDLTDSTVLRNLGVGIGYALIAYQSTLKGVSKLEVNRDHLLDELDHNWEVLAEPIQTV
MRRYGIEKPYEKLKELTRGKRVDAEGMKQFIDSLALPEAEKTRLKAMTPANYIGRAVT
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AAYPEVDWHQFSEEEVTSLGIQWNPYTTQIEPHDYIAELFDCIARFNTILIDFDRDVW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Coding sequences below are predicted from manually evaluated computer analysis, using similarity information and the programs; GLIMMER; http://www.tigr.org/softlab/glimmer/glimmer.html and GeneMark; http://opal.biology.gatech.edu/GeneMark/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EC numbers were kindly provided by Junko Yabuzaki and the Kyoto Encyclopedia of Genes and Genomes; http://www.genome.ad.jp/kegg/, and Pedro Romero and Peter Karp at EcoCyc; http://ecocyc.PangeaSystems.com/ecocyc/
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                              Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (29-WAR-2001) Genome Sequencing Center, Department of Genetics, Washington University School of Medicine, 4444 Forest Park Boulevard, St. Louis, MO 63108, USA COMMENT Supported by NIH grant 50 01 AI43283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="similar to E. coli adenylosuccinate lyase (AAC74215.1); Blastp hit to AAC74215.1 (456 aa), 94% identity in aa 1 - 456"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://kinich.cifn.unam.mx:8850/db/regulondb_intro.frameset
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The Salmonella typhimurium Genome Sequencing Project.
Direct Submission
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/organism="Salmonella typhimurium LT2"
/strain="LT2; SGSC 1412; ATCC 700720"
/db_xref="ATCC:700720"
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/product="adenylosuccinate lyase"
                                                                                                                                                                                                                                                                                                                      Nature 413 (6858), 852-856 (2001) 21534948
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/note="LT2"
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   Salmonella typhimurium LT2
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                                                                                                                                                                                                                                                                     /translation="MKPGAFGYLPMNKTTEYIDAMPIAASEKAALPKTDIRAVHQALD
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VATWYMKTILPYGGRALINEDMOWQDLWYSEMOLLPYMLQTGILILFAVLECWYSAG
FWTALMGFLQLLIGRDKYSISASTVGDEPLNPEHRTALIMPICNEDVNRYFACLRATW
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VULAPYRKLFHTYVEYVSAFLGRWSYWLAYDLSTALLIWCKGTKEVGGFWRYTLSLLLEVLFS
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TDRFLEMNRGSLDGGFWHANSFNARAFRHRAGSVLEIRBEGGLNG
TPEKLNRDRRLVILSDPVTMARLHFRWWNSPERYSSWVSYYEGIKLNPLARRFDAAS
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DGDIMWQVEFFADEGEEGECLPMLSGEAAQSVFDGDYDEIEIRQEWQEENTLHEWDEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation-**MELIVYSIMVTLLSGCGSIISRTIPGGGHGNQYYPGVQMDVRDS
AWRYVTLLDLPFSLVFDTLLLPIDIHHGPYE"
complement(8060. 8437)
            /note="similar to membrane glycosyltransferase MDOH_ECOLI
gi[1787287 percent identity 100 in 847 as but differs at
N-ter (Conserved in E.coli K-12)"
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/note="similar to MSYB_ECOLI gi|1787289 percent identity
99 in 125 aa (Conserved in E.coli K-12)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="identical to YCEK_ECOLI gi|1787288 (Conserved in E.coli K-12)"
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                                                                                                                                     /evidence=not_experimental
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/transl_table=11
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/evidence=not_experimental
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complement(8060, .8437)
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Salmonella typhimurium LT2.
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7832, .8059
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/gene="ECs1428"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NKPYDVLPQFTDEAGRRTLKDF1PVQGVYAAGRLDRDSEGLLVLTNDGALQARLTQPG
KRTGK1YYVQVEG1PDNAALQALRTGVTLNDGPTLPAG1E1VAEPDWLWPRTPP1RER
KN1PTSWLKVTLYEGRNRQVRRMTAHVGHPTLRL1RYSWGDYTLNGLDNGQWRE1AQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BCT 06-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 254050 bp DNA linear BCT 06-JUN-200 Salmonella enterica serovar Typhi (Salmonella typhi) strain CT18, complete chromosome; segment 5/20.
AL627269 AL513382
AL627269.1 GI:16502231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="putative ribosomal large subunit pseudouridine synthase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note-"putative RBS for STM1236; RegulonDB:STMS1H001492"
1740. .4754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Salmonella.
1 (bases 1 to 254050)
Parkhill, J. Dougan, G., James, K.D., Thomson, N.R., Pickard, D., Parkhill, J., Churcher, C., Mungall, K.L., Bentley, S.D., Holden, M.T.G., Sebaihia, M., Baker, S., Basham, D., Brooks, K., Chillingworth, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Salmonella enterica subsp. enterica serovar Typhi.
Salmonella enterica subsp. enterica serovar Typhi
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
.....- putative RBS for ymfB; RegulonDB:STMS1H001491"
complement(3822, .4159)
/gene="STM1236"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein
aa), 83%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="putative binding site for FruR, RegulonDB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="similar to E. coli orf, hypothetical (AAC74219.1); Blastp hit to AAC74219.1 (207 identity in aa 1 - 205"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 22; DB 1; Length 24578;
Pred. No. 0.8;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="putative -35_signal for icdA; RegulonDB:STMLTH004480"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(4148. .4813)
/gene="ymfC"
                                                                                                                                                                                                                                                                                                                                                                                         complement(4148. .4813)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(4154. .4159)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /bound_moiety="FruR"
4829, .6235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Pr
tive 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note-"STM1238"
4829. .4837
                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="STM1237"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="STM1236"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71 AGCGATTCAGCTCACGACAAGC 92
                                                                                                                                                                                    /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STMS1H000184"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1829. .4837
/qene="icdA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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Best Local Similarity
Matches 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein_bind
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                                                                              gene
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KEYWORDS
SOURCE
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                                                                                                                              CDS
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//docolement(1467...1472)
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DGNKDQSYFLYTLGHEQIAQSLFPVGELEKPQVRKIAEDLGLVTAKKKDSTGICFIGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="G1:16419754"
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complement(3815. .3820)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RKFRDFLGRYLPAQPGKIITVDGDEIGEHQGLMYHTLGQRKGLGIGGTKDGSEDPWYV
VDKDVENNVLIVAQGHEHPRLMSVGLIAQQLHWVDREPFTGTLRCTVKTRYRQTDIPC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="ycfc"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="trmu"
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complement(3349, .3820)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="trmu"
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/note="similar to E. coli orf, hypothetical protein
(AAC74217.1; Blastp hit to AAC74217.1 (383 aa), 94%
identity in aa 1 - 383"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="%imilar to E. coli putative phosphohydrolase (AAC74218.1); Blastp hit to AAC74218.1 (153 aa), 84% (Gentily in aa 1 - 152" (codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="putative MutT-like protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="putative -10_signal for ycfC;
RegulonDB:STMLTH004479"
complement(2152. .2160)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for yefc,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="putative -35_signal
RegulonDB:STMLTH004479"
complement(2189. .3349)
                                                                                              complement(1461. .2108)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(2112. .2117)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(2134. .2142)
                                                                                                                                                                                                                                                        /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="trmU"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="STM1235"
                                                                                                                                                                                                                                  /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="ymfB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="ymfB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="ycfC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="ycfC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -10_signal
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                        gene
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TITLE JOURNAL

COMMENT

gene

FEATURES

CDS

AUTHORS

REFERENCE

MEDLINE PUBMED

JOURNAL

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FITARQFPQMVRFTPSPLHDGLHLTAPDGSSALVRFTDFTPQDAPTEVWGNHFTARVA
PTAINOWLSGFFSRDVQLCWVGPQLTRRVKRHNAVPLGFADGYPYLLTNBASLRDLQQ
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LDDSYTPEKHPGSYTJDWQGOTFCONNQOVLLEQLENGGIRIPYSCRAGICGCCRIR
LLEGEVSPLKKSAMGDDGTILSCSCVPKTALRLEN"

complement(4737. . 4955)
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                                                                                                                                                                                                                                   KVYAYAGYIAINISSPNTPGLRTLQYGDALDDLLTAIKNKONDLQVIHHKYVPVAVKI
APDLCEEELIQVADSLLRHNIDGVIATNTTLDRSLVQGMKNCQQTGGLSGRPLQLKST
EIIRRLSLELKGQLPIIGVGGIDSVIAAREKIAAGATLVQIYSGFIFKGPPLIKEIVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="conserved hypothetical protein"
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TCBW_ECOLI (192 aa), 90% identity in 180 aa overlap. Note
discrepency in position of translational start site."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Pfam match to entry PF00111 fer2, 2Fe-2S iron-sulfur cluster binding domains, score 55.90, E-value
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(4716. .5825)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.46-165"
3238. 33297
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Dihydroorotate dehydrogenase, score 563.50, E-value
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5924. .8032
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                           3136. 3990
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5924. .8(
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Connerton, P., Cronin, A., Davis, P., Davies, R.M., Dowd, L., White, N., Feltwell, T., Hamlin, N., Haque, A., Hien, T.T., Holroyd, S., Jagels, K., Krogh, A., Larsen, T.S., Leather, S., Moule, S., O'Gaora, P., Parry, C., Quail, M., Rutherford, K., Simmonds, M., Skelton, J., Stevens, K., Whitehead, S. and Barrell, B.G. Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18

Nature 413 (6858), 848-852 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RVAQGELENGRHWVQWQDPFPKPCYLFALVAGDFDVLRDTFTTRSGREVALELYVDRG
NLDRAWWARTSLKNSKWRDPFPRGLEYDLDIYHYAVDPFRWAGAMENKGALIFNSKYY
LARTDTATDKDYLDTERVIGHEYFHWYTGPRYTCROWFOLSIKEGLTYPFROGESSDL
GSRAVNRISNVRTMRGLQFAEDASPWAHPIRPDKVIEMNNFYTLTVYEKGAEVIRHIH
KLÜGENRFQKOMQLYPERHOSGAATCDDFVQAMEDASIWDLSTIFRRWYSGSGFPITVY
KDINNFTGERGYTLTSQRTPATADQAEKQBLIIPFAELXDNBGNYPLQKGGHPVNA
VLNNYTQAEQTFTFTISQRTPATADQAEKQBLIIPFAELXDNBGNYPLQKGGHPVNA
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/note="Pfam match to entry PF01433 Peptidase_M1, Peptidase
family M1, score 245.10, E-value 1.9e-84"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="wTQQPQAKYRHDYRAPDXQITDIELTFDLDAEKTVVTALSQAVR
HGAPDAPLRLDGEDLTLVSIHVNDAPWTAYKEEGGALIISDLPERFTLRIVNEISPAA
NTALEGLYQSGDALCTQCEAEGFRHITWYLDRPDVLARFTTKIIADKSKYPFLLSNGN
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IAELFEVIDPIAIAQVREALTRTLAAELADEFLAIYNANHLDEYRVDHGDIGKRTLRN
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QOGGLYMDKWFTLQSTSPAENVLETYRSLLKHRSFSMSNPNRIRSLIGAFRGSNPAAFH
AQDGSGYQELVEMLTDLNSRNPQVASRLIEPLIRLKRYDDKRQEKMRAALEQLKGLEN
LSGDLYEKITKALA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Orthologue of E. coli pepN (AMPN_ECOLI); Fasta hit to AMPN_ECOLI (869 aa), 94% identity in 869 aa overlap" /codon_start=1 /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Details of S. typhi sequencing at the Sanger Centre are available on the World Wide Web.
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                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (25-CTT-2001) Submitted on behalf of the Salmonalla
Sequencing team, Sanger Centre, Wellcome Trust Genome Campus,
Hinxton, Cambridge CB10 15A, UK
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Location/Qualifiers
1. .254050
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/protein_id="CAD08183.1"
/db_xref="G1:1650233"
/db_xref="SPTREMBL:Q827T0"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E-mail: parkhill@sanger.ac.uk
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/gene="STX1078"
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/gene="STY1079"
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/gene="STX1079"
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Parkhill, J.
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1060. .108
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                                                                                                                                 FEATURES
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BOQKARORLEDITAEKWARQEGETYLYDDELPEYNVAVDRYGDWAVIGEYAPRIV
DAQKARORLEDITAEKURTISVLGIPPOKILVLKTREROKOKNOYOKMSEKGEFLENSEYNA
RLWVNLTDYLDTGLELDHRIARRMLGEMSKGKDFLNLFSYTGSASVHAGLGGARNTTT
VDMSRTYLEWARRNIERINGLSSRAHRLIQADCLGWIKREANBOPDLIFTDPPFFSNSKR
MEESFDVQRDVALMKDLKRLIRKGGTIMFSNNKRGFRMDLEGLAELGLTAQEITQKT
LSPDFARNRQHNCWLIRAA"
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                                                                                                  /translation="MNSLFASTARGLEELLKIELEKLGAVGCQVVQGGVHFQGDTRLI
YQSLAWSRLASRIILPWGECKVYSDLDLYFGVQAINWTEIFNPGATFAVHFSGLNDTI
RNSQYGAMKVKDAIVDAFTRKNLPRPNVDRESPDLRINVWLNKETASIALDLSGDGLH
                                                                                                                                                                                                           HRGHWGFSGWAQHDEAIWQEVKAEAQTRARKGLAEYSSHFYGSDSDARVIERARSNAR
RAGIGELITFEVKDVAQLSNPLPKGPYGTVISNPPYGERLDSDPALIALHSLLGRTMK
NQFGGWNLSLFSASPDLLGSLQLRADKQFKAKNGPLDCVQKNYHIAETTĄDSKPATVA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Fasta hit to YBIT_ECOLI (530 aa), 32% identity in 526 aa overlap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fasta hit to VJJK_ECOLI (554 aa), 34% identity in 524 aa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Orthologue of E. coli UUP_ECOLI; Fasta hit to UUP_ECOLI (635 aa), 94% identity in 634 aa overlap" /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6506. .6541
/gene="STY1082"
/note="PS01261 Uncharacterized protein family UPF0020
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Liss,P., Perna,N.T., Rose,D.J., Mau,B., Zhou,S., Schwartz,D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                //orde="Pfam match to entry PF01170 UPF0020,
Uncharacterized protein family UPF0020, score 781.30,
E-value 3.7e-231"
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/product="ABC transporter ATP-binding protein"
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llarity 100.0%; Pred. No. 1;
Conservative 0; Mismatches 0; Indels 0
'product="conserved hypothetical protein"
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J. Bacteriol. 184 (16), 4601-4611 (2002)
                        /protein_id="CAD08187_1"
/db_xref="G1:16502236"
/db_xref="SPTREMBL:Q827S6"
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/gene="STX1082"
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/gene="STY1083"
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/gene="STY1083"
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Yersinia pestis KIM
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Best Local Similarity
Matches 22; Conserv
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VERSION
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AE013675
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/note="residues" 5 to 712 of 712 are 86.31 pct identical to residues 5 to 712 of 712 are 86.31 pct identical to residues 5 to 712 of 712 are 87.16 pct identical to residues 5 to 712 of 712 from GenPept : >glAaL23272.11 (AE008908) anaerobic ribonucleoside-triphosphate reductase [Salmonella typhimurium LT2]"
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/db_xref="G1:21957455"
/db_xref="G1:2195745
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ITARVAPILYWGAGGVRLQADDNIAEIFKNGRASISLGYIGIHETINALFGHQTHLF
DDQKLREKAIAIVAHLKQATDDWNDETGYAFSLYSTPSENLCDRFCRLDTAEFGVVEG
VTDKGYYTNSFHLDVEKKVNPYDKLDFEAPYPPLANGGFICYGEYPNLQHNIRALEDV
WDYSYSRVPYYĞINTPIDECYEGGFTGEFSCTSKGFTCPKCGNHEPSKVSVTRRVGGY
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QRTLGEPLKIHGEKNIAQRIAQALEQVGLPASAALRYPHQFSGGQRQRIAIARALLLR
PKLLLLDEPTSALDMSVQAETLNLLNHLKREYGMTYLLVSHDSDVVAHMSERAVLMEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /transī_table=11
/product="anaerobic ribonucleoside-triphosphate reductase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /function="transport of large molecules: protein, peptide secretion"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /function="transport; protein, peptide secretion"
/note="residues 14 to 276 of 302 are 42.06 pct identical
to residues 2 to 258 of 327 from E. coli K12: B3541;
residues 11 to 295 of 302 are 43.64 pct identical to
residues 1 to 277 of 278 from GenPept: >dbj|BAB51953.1|
(AP003006) oligopeptide ABC transporter, ATP-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="residues 3 to 230 of 238 are 50.64 pct identical residues 1 to 226 of 245 from GanPept : ydplAA145414.1| (AE009390) ABC transporter, nucleotide binding/ATPase protein [dipeptide] [Agrobacterium tumefaciens str. C58 (U. Washington)]"
                                                                                                                                                                                                              University of Wisconsin, 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /function="enzyme; 2'-Deoxyribonucleotide metabolism"
Fetherston, J.D., Lindler, L.E., Brubaker, R.R., Plana, G.V., Straley, S.C., McDonough, K.A., Nilles, M.L., Matson, J.S., Blattner, F.R. and Perry, R.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Yersinia pestis KIM"
                                                                                                                                                 Direct Submission
Submitted (21-FEB-2002) Genetics, U
Henry Mall, Madison, WI 53706, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(3409. .4317)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /strain="KIM"
/db_xref="taxon:187410"
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/gene="nrdD"
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AFLPAGTDEKHVVLQTGDFVVFFPGEVHKPLCAVGEPANVRKAVVKIAVK"
complement(9251. .10258)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MNOFYKRHFLRLLDFTPABITALLDLATELKKDKKSGCEQQKLV
GKNIALIFEKDSTRTRCSFEVAAYDQGARVTYLGPGGSQIGHKESIKDTARVLGRMYD
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YLGDFRNNMGNSLLEAAALVGMDLRLVAPKACWPEERFYISCQALAQKTGGKITLTED
IAEGVNGADFLYTDVWVSMGEPKEVWDERINLKPYQVNMRVLTLTGNRQVKRILLTED
AFHDDQTTIGKQMAEQYDLPGGMEVTBEVFESAHSIVFDQAENRLHTIKAVMVATMSK
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Yersinia pestis strain CO92 complete genome; segment 17/20.
AJ414157 AL590842
AJ414157.1 GI:15981328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Parkhill, J., Wren, B.W., Thomson, N.R., Titball, R.W., Holden, M.T.G., Prantice, M.B., Sebaihia, M., James, K.D., Churcher, C., Mungall, K.L., Baker, S., Basham, D., Bentley, S.D., Brooks, K., Cerdeno-Tarraga, A.M., Chillingworth, T., Cronin, R., Davies, R.M., Davis, P., Dougan, G., Feltwell, T., Hamlin, N., Holroyd, S., Jagels, K., Leather, S., Karlyshev, A.V., Moule, S., Oyston, P.C.F., Quail, M., Rutherford, K., Simmonds, M., Skelton, J., Stevens, K., Whitehead, S. and Barrell, B.G. Genome sequence of Yersinia pestis, the causative agent of plague Nature 413 (6855), 523-527 (2001)
                                                                                                                                                                                                                                                                                                                                                                       /function="enzyme; amino acid biosynthesis: Arginine" //functerresidues 1 to 334 of 335 are 79.64 pct identical transidues 1 to 334 of 334 from E. coli K12: 84254; residues 1 to 334 of 335 are 79.94 pct identical to >99|AAG59453.1|AR005657.13 (AR005657) ornithine carbamoyltransferase 1 [Escherichia coli 0157:H7 EDL933]"
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Submitted (04-OCT-2001) Submitted on behalf of the Yersinia
sequencing team, Sanger Centre, Wellcome Trust Genome Campus,
Hinxton, Cambridge CB10 1SA E-mail: parkhill@sanger.ac.uk
Notes:
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/transl_table=11
/product="contihine carbamoyltransferase 1"
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/db_xref="G1:21957461"
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Pred. No. 2.9;
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                                                                                                                                                                                                                                                                                                                                               /gene="argi"
/function="enzyme;
/note="residues 1 t
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                                                                                                                                                                                                                                                                                          /note="y0740"
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Best Local Similarity
Matches 21; Conserv
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AJ414157/C
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VERSION
KEYWORDS
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JOURNAL
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TITLE
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/function="transport; protein, peptide secretion"
/note="residues 2 to 275 of 278 are 42.29 pct identical to
residues 18 to 296 of 300 from E. coli K12: B3542;
residues 18 to 275 of 278 are 59.07 pct identical to
residues 47 to 305 of 310 from GenPept: >emb|CAC46990.1|
(ALS91790) putative dipeptide transport system permease
ABC transporter protein [Sinorhizobium meliloti]"
                                                                                                                                                                                                                       LVGESGSGKSITARALMGLVRHPGKVSAKKLSYXSDWTDDQGHSGOITETHDLINNY
OWSALRGSETAMVLODPRYALNPVQPVGKQIEESLLLHNTLSSADAHERVLNALASVG
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TEQRMSLLLISHDLPLVABEHCHRVLWYQGKLVDQGLAADLPHSTHPYTHTLWACRP
NAHTYGTDLPYLDRSYDFSGGSRGTD*
COMPLEMENT (4280. 5116)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="WILLEPERTLKRSPSTSIGLFILSLIVIIAVFAPWLAPDDPNWO NAADKLLPPGDSGHLLGTDSYGRDMLSRLIYGTRPTIGLVLLYTTLPLGLLVGVLS GYYGGWLERILMRITDVVMSWPRILIAFAFYAMLGFGLLNGALALTTWPAYARQAR GYYGGWLERSDYLAAAEMMGIRGLRLIMGHILPMCLPSAVVRLALDLAGIILAAAGLGFLGGARPPMSEWGSMVADGMQVIFDQWWIAAIPGCAILLSSNAFNLLGDGLRDILDPHHD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MGYALNTTPGTPSRRHLLVFLQGLFTLALTLFGLLVITFFLSAL
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WLGLLALLLFYARLQDYGYGPGFLDDIYQYFVGAKTGFVLDTWRSGDMGAFNNALGHN
ILPVSLLAYYALASITRLTRSACLSELNKEYITLARAKGAGBHRILLHHVLDNIRGTL
LTVIALAYTSALEGAVLTETVFAWFGIGRYLTSALFAGAGTAINGGTLLLGMYCFILIN
                                                                                                                                                                                               /translation-"MAYAIFWILTMTDSIFTVDNLCVDFQQQRVVDNISFHLGHERVA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="residues 19 to 347 of 349 are 44.68 pct identical to residues 6 to 333 of 340 from E. coli K12: B1486; residues 13 to 348 of 349 are 48.51 pct identical to residues 13 to 348 of 349 are 48.51 pct identical to ALS91790) putative dipeptide transport system permease ABC transporter protein [Sinorhizobium meliloti]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="dipeptide transport system permease protein
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                                                                         /product="putative ATP-binding component of dipeptide transport system"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="putative transport system permease protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="y0737"
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protein [Mesorhizobium loti]"
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                                                                                                                                                                                                                                                                                                                                                                                               /gene="dppc"
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complement(4280. .5116)
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/gene="y0737"
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8486. po.
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/gene="y0739"
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                                                                                                                                                                                                                                                                                                                                                                       gene
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AVFAKTFDDISLVPFFVLTPLTYLGGVFYSLSLLPPPWQAVSKLNPIYYMISGFRYGF
LGITDVSLAYTIGVLVVFIAVFYAMAMYLIERGTGLRT"
                        RFLNTSTTTSDVAFSNQMAYLKQAGYDTISLYQLBGYLNNKINLPAKVVVLTFDDGLK
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     AENLRYPIVGKLKDRLSNTWYQVNIGDRLGYVSSADAEIDNGIPILTYHHMLKNEENK
                                                                                                                                                                                                                                                                                                          protein in hpt-panD intergenic region radH SW:YADH_ECOLI (P36880) (256 aa) fasta scores: E(): 0, 80.1% id in 256 aa, and to Vibrio cholerae putative permease Vc0590 TR:O9KUDZ (EMBE:AE004144) (256 aa) fasta scores: E(): 0, 66.0% id in 256 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 predicted
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                                                                                                                                                                                                                                                                                    /note="Similar to Escherichia coli hypothetical 28.5 kDa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Pfam match to entry PF01061 ABC2_membrane, ABC-2 type transporter, score -22.30, E-value 5.8e-05" complement(3427. 3492)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 predicted
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(P36879) (308 aa) fasta scores: E(): 0, 81.8% id in 308
aa, and to Vibrio cholerae ABC transporter ATP-binding
protein VcoS99 TR:0980D3 (EMBL:AE004144) (305 aa) fasta
scores: E(): 0, 71.4% id in 304 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="putative ABC transporter, integral membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note-"PS00890 ABC-2 type transport system integral membrane proteins signature." complement(3592. .3657)
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for YPO3405 by TMHMM2.0"
complement(3526. .3639)
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/note="one of 6 probable
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for YPO3405 by TMHMM2.0"
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for YPO3405 by TMHMM2.0"
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for YPO3405 by TMHMM2.0"
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/gene="xPO3405"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for YPO3405 by TMHMM2.0 complement(3919. .3984)
                                                                                                                                                                                                                               complement(3400. .4170)
/gene="YPO3405"
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                                                                                                                                                      .4170)
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                                                                                                                                                      complement(3400.
/gene="YPO3405"
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/transl_table=11
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                                                                                                                                                                                                         /note="yadH"
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                                                                                                                                   VIEMD"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation-"MLITETLPLERQQIRRWRQBGGKRIALVPTWGNLHEGHWTLVDEA
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LEKGYNDWGYDINYDVTVRARDLESSRNGYLTEERQAIPQLSK IMWALLE
ERQIDALLEERAAQLLRVGFTPDELFIRDAFTLQPLTVDSQQAVILMAAMLGKERMAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pseudomonas aeruginosa aspartate 1-decarboxylase precursor Pa4731 TR:AAG08117 (EMBL:AE004887) (126 aa) fasta scores: E(): 1.5e-27, 58.2% id in 122 aa" /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Pfam match to entry PF02261 Asp_decarbox, Aspartate decarboxylase, score 264.30, E-value 1.6e-75" complement(1880. .3073)
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NGTGFIDKDDLREINKAQKNNDMLGDLNKPLPNQNILTMREAKVYLAADVRSEQFAVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (EMBL:AE004144) (293 aa) fasta scores: E(): 0, 59.0% id in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Similar to Escherichia coli hypothetical protein
YadE SW:YADE_ECOLI (P31666) (409 aa) fasta scores: E(): 0,
65.4% id in 382 aa"
                                                                                                                                                                                                                                                                                                                                                                                     /note="Similar to Escherichia coli pantoate-beta-alanine ligase Panc Sw:PANC_ECOLI (P31663) (283 aa) fasta scores: E(); 0, 72.0% id in 282 aa, and to Vibrio cholerae pantoate-beta-alanine ligase Vc0591 TR:Q9KUDI
Details of Y. pestis sequencing at the Sanger Centre are available on the World Wide Web.
                                                (URL, http://www.sanger.ac.uk/Projects/Y_pestis/).
Location/Qualifiers
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| db_xref="GI:15881329"
| db_xref="SPTREMBL:082BK7"
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                                                                                                                                                                                                            /note="biovar: Orientalis"
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/note="panD"
1351. .1731
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/transl_table=11
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/gene="YPO3403"
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                                                                                                                                                                                                                                                          /gene="YPO3402"
                                                                                                                                                                                                                                                                            /note="panc"
86. .940
                                                                                                        .216050
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Gaps . 0 BCT 05-JUL-2001

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1 171 c 183 t 131 g 283 t
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FERTHGTARKXAGONKNPGGIILSAEMMLRHMGWTEAADLIVKGMEGAINAKTVTV
                                                                                                                                                                                                                                                                                                                                                                                               ABO64593 7770 bp DNA linear BCT 05-JUL-200
Escherichia coli icdA gene for isocitrate dehydrogenase, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aoshima,M., Ishii,M., Yamagishi,A., Oshima,T. and Igarashi,Y. Squence polymorphism around the isocitrate dehydrogenase (ICDH) gene of Escherichia coll BL21(DE3) and citrate accumulation of an ICDH defective derivative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (03-JUL-2001) Miho Aoshima, The University of Tokyo,
Submitted (03-JUL-2001) Miho Aoshima, The University of Tokyo,
Graduate School of Agricultural and Life Sciences; Yayoi 1-1-1,
Bunkyo-ku, Tokyo 113-8657, Japan
(E-mail:aomiho@mail.ecc.u-tokyo.ac.jp, Tel:81-3-5841-5143,
Fax:81-3-5841-572)
Location/Qualifiers
1. 7770
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/protein_id="BAB61874.1"
/db_xref="G1:14624985"
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                                                                                                                                                  3.0%; Score 20; DB 8;
00.0%; Pred. No. 8.5;
ve 0; Mismatches
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100.0%; Pred. No. 11;
tive 0; Mismatches
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/db_xref="GI:19310942"
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1138. .2388
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100.0%; PA.
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/transl_table=11
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AB064593.1 GI:14624984
                                                                                                                                                                                                                                           323 GAAAATTTACTATGTGCAG 342
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1138. .2380
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/gene="icdA"
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Aoshima, M.
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Matches 20; Conserv
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AB064593/c
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                                                                                    BASE COUNT
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SOURCE
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DEPPRACVIELRRSWAGFKELNAGOTTILTTHYLEBAEMICRNIGIIONGELVENY
TWKOLLSKLESETTFTPLGAKSPLERYGYRLTHYLEBAEMICRNIGIIONGELVENY
VQCVQVQSMRNKANRLEELFVTLVNGHEGEKA"
VQCVQQSMRNKANRLEELFVTLVNGHEGEKA"
/gene="YPO3406"
/note="Pfam match to entry PF00005 ABC_tran, ABC
transportery, score 198.80, E-value 8.5e-56"
/gene="rp03406"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ar415022 884 bp DNA linear PLN 10-WAR-2002 Chamaebatlaria millefolium isolate 90Chamaebatlar NADP dependent sorbitol 6-phosphate dehydrogenase gene, partial cds. AF415022
               /product-"putative ABC transporter, ATP-binding protein"
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/tb_xref-"SPTREME.:QBCBK3"
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STIGIISSLVNKTSGKVQVFGYDIDNDIVNAKRQLGLVPQEFNFNPFETVLQIVITQ
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Rosales; Rosaceae; Rosaceae incertae sedis;
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Bortiri, E., Oh, S.-H., Gao, F.-Y. and Potter, D.
Phylogenetic analysis of Prunus (Rosaceae) as determined by sequences of s6pdh
                                                                                                                                                                                                                                                                                                                                                                    /note "PS00211 ABC transporters family signature."
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join(<223. .442,656. .>884)
/product="NADP dependent sorbitol 6-phosphate
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/isolate="90Chamaebatiar"
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Submitted (29-AuG-2001) Pomology, University one Shields Ave, Davis, CA 95616, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                    'note-"PS00017 ATP/GTP-binding site
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/codon_start=2
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                                                                                                                                                                                                                                                                                                                                                                                      complement(4959. .4982)
/gene="YPO3406"
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/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                        5329. .5991
/gene="YPO3407"
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/gene="YPO3407"
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Matches 21; Conservative
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VERSION
KEYWORDS
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AF415022
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TITLE
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Gaps

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/transl_table=11
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/dene="1796"
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PDAIIDLGLGEDGLGLIRRWRSHQENLPILVLTARESWGDVRVAVER
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LIRNAGKVVSKDTLMLQLYPDAELRESHTIDVLMGRLRKKLLAEHQGEVITTIRSQGY
                                                                                                                        /translation="MLRKNNKPFSLRARFLMATAGVILALSLSYGMVAVVGYIVSFDK
STFRAHRGESNLFFSLAQWHNNKLSISVPPELELNVPSLVLIYDKDGNILMRQRHVPE
                                                                                                                                                                                                    LESHIEKSWLQKPGFYELDTGTHISRMMGDNPKAQDQLKKYDDTDDSALTHSVSVNT
YAATSRLPQLTIVVVDTIPQELQRTDLVWNWFSYVLLANLLLVIPLLMLAAYWSLRPI
KALASQISQLEKGEREQLDENPPRELQSLVRNLNILLMNERQRYTKYRTTLADLTHSL
                                                                                                                                                                                                                                                                                                                KTPLAVLOTTLKSLRTGKQTT1EEVEPIMLEQISRISQQIGYYLHRASMRSEHNVLGR
EHSVPALLIDSLYSALMKVYQRKGLATTLDISPEVTFLGEKNDFMEVMGNVLENACKY
CLEEVEVTTLHSEKQLTIVVDDDGFGIPENKRQLIFQRGQRVDTLRPGGGLGLSIAAE
IIEQYQGKISITESPLGGARMMVTFGQQDCHDD"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /function="regulator; global regulatory functions"
//note="residues 1 to 222 of 223 are 81.08 pct identical residues 1 to 222 of 223 from E. coli K12 : B1130;
residues 1 to 223 of 223 are 100.00 pct identical to residues 1 to 223 of 223 are 6100.00 pct identical to residues 1 to 223 of 223 from GenPept : >emb|CAC90456.1|
(AJ414149) response regulator protein [Yersinia pestis]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="residues 84 to 207 of 207 are 27.61 pct identical to residues 105 to 238 of 238 from GenPept : >emb|CAA79374 11 (218941) outer membrane protein [Neisseria gonorrhoeae]"
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gene_id:K23F3.8
similar to unknown protein [Arabidopsis thallana]"
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/protein_id="sensor protein Phog"
/protein_id="AAM83361.1"
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/translatit
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/gene="y1795"
/gene="y1795"
/gene="y1795"
/function="unknown"
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/gene="phop"
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/gene="y1796"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(2812. .3483)
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/gene="purB"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="phop
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                                                                                                                        Yersinia pestis KIM section 182 of 415 of the complete genome.
AE013782 AE009952
AE013782.1 GI:21958600
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/product="hypothetical protein"
/db_xref="c1:21958601"
/db_xref="c1:21958601"
/db_xref="c1:21958601"
/translation="magirylingFHLYPGINMDYQLDLDWPDFLQRYWQKRPVILKR
GFRWFIDPLSPDELAGLAMENEVDERLYSHEDGRWHYSHGFPESEDHLGENNWSLLVQ
AVDHWHEPAALMRPFRELSDWRMDDLMISFSVPGGGGVGPHFDQYDVFIGGRNWSCRRW
RVGEKTEMKOHCPHPDLLQVGPFDAILDEEWBFGDILYIPPGFPHEGYSLENALNYSV
QOPEHFQNWFGEFISQSRHELDIAPPEPPYQTGDILREHPABYLPSSYDKLRTWMLDLV
QOPEHFQNWFGEFISQSRHELDIAPPEPPYQTGDIYELLKQGDELQRLSGLRVLRVGD
RCFANGELIDPFHLQAANALCQHFSVNAEMLGDALEDPSFLAMLAALVNSGYWYFND"
complement(1352..2806)
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/note="residues 17 to 389 of 391 are 79.08 pct identical
to residues 2 to 374 of 376 from E. coli Kl2 : B1128;
residues 17 to 389 of 391 are 79.08 pct identical to
residues 2 to 374 of 376 from GenPept :
>9b|AAG5593-11AED05327_2 (AED05327) orf, hypothetical
protein [Escherichia coli 0157:H7 EDL933]"
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1 (Dases I to 10473)

2 (Dases I 
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Deng, W., Burland, V., Plunkett, G. III, Boutin, A., Mayhew, G.F., Liss, P., Perna, N.T., Rose, D.J., Mau, B., Zhou, S., Schwartz, D.C., Fetherston, J.D., Lindler, L.E., Brubaker, R.R., Plana, G.V., Straley, S.C., McDonough, K.A., Nilles, M.L., Matson, J.S., Blattner, F.R. and Perry, R.D.
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/function="enzyme; global regulatory functions"
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J. Bacteriol. 184 (16), 4601-4611 (2002)
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/db_xref="taxon:187410"
complement(147. .1322)
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/transl_table=11
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/note="y1793"
        837 TTCAATAAACCCTACGATGT 818
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Yersinia pestis KIM
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                                                                            SOURCE
/function="enzyme; purine ribonucleotide biosynthesis" note="residues 4 to 459 of 459 are 88.59 pct identical to residues 1 to 456 of 456 from E. coli K12: B1131; residues 1 to 456 of 459 are 88.59 pct identical to residues 1 to 456 of 456 from GenPept:

>9b|AAG5957.1|AE005329.1 (AE005329) adenylosuccinate lyase [Escherichia coli 0157:H7 EDL933]"
                                                                                                                                                                                                                                                                                                                                             LKEKVENLPALHAVSEFIHFACTSEDINNLSHALMLQTARODVLLPAWROIIDSIKAL
AHQYRDLPLLSRTHGQPATPSTIGKELANVAYRMERQFRQLTQVEILGKINGAVGNYN
AHIVAYPEVDWHQFSESFVTSLGINWNPYTTQIEPHDYIAELFDCVARFNTILIDFDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MIVAKNYYDITLALAGICQSARLVQQLAHEGQCDNDALNTVLRG
LLQTNPRSSTLAVYCOTEQVLKMGLETLQSYLNANRQGEAABLTRYTLSLAVLERKLSA
SKAAMYLGERISQLDRQLHFDLESETMMSSLASIYVDVVSPLGPRIQVTGSPAILQ
SPLVQAKYRATLLAGILSAYLWQQVGGSRLQLMFSRNRLFKQAQSILAHT"
complement(6620. .7735)
                                                                                                                                                                                                                                                                                                                                                                                                                       DIWGYIALNHFKQKTIAGEIGSSTWPHKVNPIDFENSBGNLGLSNAVIGHMASKLPVS
RWQRDLTDSTVLRNLGVGLGYALIAYQATWKGISKLEVNEAHLLQELDHNWEVLAEPI
QTIMRRYGIEKPYEKLKELTRGKRVDAAGWQAFIDGLDLPEEEKNRLKAMTPANYIGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="y1798"
/note="residues 3 to 209 of 210 are 75.48 pct identical to
residues 1 to 208 of 213 from E. coli K12 : B1132"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="residues 7 to 367 of 371 are 87.53 pct identical to residues 21 to 381 of 383 from E. coll K12: B1133; residues 1 to 371 of 371 are 100.00 pct identical to residues 1 to 371 of 371 from GenPept: >emb|CAC90460.1|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MSDNSQKKVIVGMSGGVDSSVSAYLLQQQGYQVAGLFMKNWEED
DDEEYCSAATDLADAQAVCDKLGMELHTVNFAAEYWDNVFELFLAEYKAGRTPNPDIL
CNKEIKKFAFLEFAAEDLGADYIATGHYVRRQDVOGKSRLLAEGLGGRNEDGSYFLYTLS
HEQIAQSLFPVGELEF PEWRIAGDLYIATGHYKKNETGFTGFTGFTGFRFBFLGRYLPAG
PGPIMTVDGQLVGKHQGLMYHTLGQRGGTGGTGGTGFTGBRKFRDFLGRYLPAG
GHEHPRLMSVGLVAQQLHWVDRQPYTAPFRCYVKTRYRQDDIPCTVTPLDDBRYDDRF
                                                                                                                                                                                                                                                                                                /translation="MPPMELSSLTAVSPIDGRYGDKVSALRPIFSEFGLLKFRVQVEV
RWLQKLAACAEIKEVPAFDANANAYLDKIVQEFNEQDAQRIKTIERTTNHDVKAVEYF
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                                                                                                                                                                                                                        /product="adenylosuccinate lyase"
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/protein_id="AAM85367.1"
/db_xref="G1:21958608"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="hypothetical protein"
/protein_id="AAM85366.1"
/db_xref="G1:21958607"
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/db_xref="G1:21958606"
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complement(5936 .6568)
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Best Local Similarity
Matches 20; Conserv
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U55370
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This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one m13 subclone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 University, Genome Sequencing Center, 4444 Forest Park Avenue, St. Louis, MO 63110, USA 5 (bases 1 to 32403)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (23-MAY-2002) Department of Genetics, Washington University, Genome Sequencing Center, 4444 Forest Park Avenue, St. Louis, MO 63110, USA Submitted by:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FICE: This sequence may not be the entire insert of this clone. may be shorter because we only sequence overlapping sections:e, or longer because we provide a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (01-JAN-2002) Department of Genetics, Washington
University, Genome Sequencing Center, 4444 Forest Park Avenue,
Louis, MO 63110, USA
6 (bases 1 to 32403)
                                                                                                                                                                                                                                                       Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium Science 282 (5396), 2012-2018 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (01-AUG-2001) Department of Genetics, Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genome Sequencing Center
Department of Genetics, Washington University
St. Louis , Mo 63110, USA, and
St. Entre, Hinxton Hall
Cambridge CB10 IRQ, England
email: rw@nematode.wustl.edu and jes@sanger.ac.uk
                                                                                                                             Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (17-APR-1996) Robert Waterston
4 (bases 1 to 32403)
                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 32403)
Du.Z., Le.T.T. and Kemp.K.
The sequence of G. elegans cosmid K03B4
Unpublished (2001)
3 (bases 1 to 32403)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            neighboring submissions
                                                              Caenorhabditis elegans
                                                                                                   Caenorhabditis elegans
                                                                                                                                                                                     1 (bases 1 to 32403)
Waterston, R.
   GI:1280096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Waterston, R.
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055370.1
                                                                                                                                                                                                                                                                                                                                                              99069613
                                                                                                                                                                                                                                                                                                                                                                                           9851916
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http://www.wormbase.org/db/seq/sequence?name=K03B4;class=Sequence For a graphical representation of this cosmid sequence and its analysis see:

## NEIGHBORING COSMID INFORMATION

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The 5' cosmid is F41F3, 200 bp overlap; the 3' cosmid is 2C266, 3000 bp overlap. Actual start of this cosmid is at base position 197 of K03B4; actual end is at 5381 of ZC266.
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Coding segences below are the result of integration and manual

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ONLESSLHKPLTGNOQGFVÖKTLENVÖKNPSQDDTHEFINQLADYPPTIPDSVTLHFL
KSAGVDGSDPRVTRNISLAAQKHVSDIILDAMTSARMKGLGGTKKGTKDTKYTLTEEL
LDEILKEYGHQUNTRPPYHT"
Join (21710 . 21784, 21836 . 21894, 21959 . 22223, 22280 . 22411)
                                                                                                                                                                                                                                              oin(21710. .21784,21827. .21894,21959. .22223,22280. .22411)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MPWPFTRDDDYDSDPEVQAEKEMAKKDPIGFAIDSSSLTSMKKA
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GISGCSSRKYSGYDDEMDEDFGDDEDYDHYGGQEVFDEDEEDTFVAKK"
23936. . 26161
                                                                                                                                                         /note="for a graphical representation of this gene see:
http://www.wormbase.org/db/seq/sequence?name=K03B4.3a;clas
s=Sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRI 30-MAR-2002
                                  /translation="mrflaaalllvavllatfpvtsagsridrsaawfrplpvrspg
Ysrsriggsrllprrmyrslpqudyqgmwdklidtdaqmdaen"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MNDPEQYEPSSSTESVLMPPPALPORPAAAPQVYSTLEPSVONL
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GVDGSDPRYTRMISLAAQKHVSDIILDAMTSARMKGLGQTKKGTKDTKYTLTEELLDE
ILKEYGHQNYRRPPYH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="for a graphical representation of this gene see:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MNDPEQYEPSSSTESVLMPPPALPQYFQRPAAAPQVYSTLEPSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="similar to human TATA-binding protein associated factor 30 kDa subunit (PIR:A54981); coded for by the following C. elegans cDNAs: yk70h11.5, yk331g8.3, yk331g8.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="coded for by the following C. elegans cDNAs:
yk99d5.5, yk113d4.5, yk117d8.5, yk158b11.5, yk172h12.5,
yk113d4.3, yk99d5.3, yk117d8.3, yk158b11.3, yk172h12.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AC106775 137586 bp DNA linear PRI 30-MAR-
Homo sapiens chromosome 5 clone RP11-322K12, complete sequence.
AC106775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                          /note="coded for by the following C. elegans cDNAs: yk602f4.3, yk602f4.3, yk602f4.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="Hypothetical protein K03B4.3a"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                              /product="Hypothetical protein K03B4.3b"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="Hypothetical protein K03B4.2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .22837,23253. .23470)
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Pred. No. 13;
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="GI:1280101"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3.0%; Scc.
100.0%; Pre
0;
                                                                                                    21710. .22411
/gene="K03B4.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22603. .23470
/gene="K03B4.2"
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                                                                                                                                                                                                                                                                                   /qene="K03B4.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="K03B4.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           join(22603.
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Las 20; Conserva
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VERSION
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SOURCE
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review of the following data: computer analysis using the program Genefinder (P. Green and L. Hillier, personal communication), the large scale EST projects of Yuji Kohara (communication), the large scale EST projects of Yuji Kohara (communication), the (http://www.ddbj.nig.ac.jp/celegans/html/CE_INDEX.html) and The C. elegans ORFeeme cloning project (http://worfdb.dfcl.harvard.edu/), similarity to other proteins from BlastX analyses (http://blast.wustl.edu/), sequence conservation with C. briggsae using Jim Kent's WABA alignment program (Genome Research 10:115-1125, 2000), individual C. elegans GenBank submissions, and personal communications with C. elegans researchers. tRNAs are predicted using the program tRNAscan-SE (Lowe, T.M. and Eddy, S.R., 1997, Nucl. Acids. Res., 25, 955-964).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="Hypothetical protein K03B4.6"
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KVTNFFGSIYLSINKLVAIFPLKINFLGFRKLTLAFFFIXYLDRVKNYFFENIDRYK
DSKFMLFSVKHLAYGGFVFPDGIFFWSLGLLIFPFFVNIFFRARTFRHDRYK
NFKDIKKNMALFFQIIFQDSLFFISVAFTMKMNMLIDHRFYSFFRGYLTLMQINA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="weak similarity to Xenopus dompamine D2 receptor (SP:P24628)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(join(5626. .5916,5967. .6269,6725. .6901,8300. .8587,8644. .8937,8982. .9150,10475. .10593,10697. .10741))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(join(2043. .2121,2169. .2442,2631. .2863,
3054. .3214,3258. .3340,3558. .3732))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                join(18524. .18578,19300. .19472,19521. .19556)
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/db_xref="GI:1280097"
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                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Caenorhabditis elegans"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(5626. .10741)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /chromosome="v"
/clone="K03B4"
complement(2043, 3732)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /strain="Bristol N2"
/db_xref="taxon:6239"
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Submitted (07-MAR-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
4 (bases 1 to 137586)
DOE Joint Genome Institute and Stanford Human Genome Center.
Direct Submission
Submitted (30-MAR-2002) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
On Mar 30, 2002 this sequence version replaced gi:19224868.
Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Finishing Completed at Stanford Human Genome Center
www-shgc.stanford.edu
Quality: Phrap Quality >=40 99.9% of Sequence;
Estimated Total Number of Errors is 0.1.
NOTE: This insert is not the entire sequence of the clone (entire sequence is 146.5kb). It is clipped at the overlap with AC092318.
The number of bases overlapped is 14552.
                                                                                                                                                        Submitted (12-7AN-2002) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 3 (bases 1 to 137586)

DOE Joint Genome Institute.
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Matches 20; Conservative 0;
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Mammalia; Eutheria;
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Galls, T. Grozel, N. Frago, W. Rord, J. Roger, P. P. Speter, P. Retragive, C. Garles, J. M. Garches, A. Garner, T. Garca M. Gill R. Georgel, J. H. Georgel, J. Harts, C. Harts, K. Hart, M. Havlak, P. Hawes, A. Hartandez, J. Hernandez, J. Hernandez, J. Gardson, J. R. Gardson, J. Read, S. Hallow, J. Hame, J. J. Gardson, J. R. Gardson, J. R. Harts, J. Hully, S. Hume, J. J. Gardson, J. R. Gardson, J. R. Harts, J. Hully, S. Hume, J. J. Gardson, J. R. Gardson, J. R. Harts, J. Hully, S. Hume, J. J. Gardson, J. R. Harts, J. Hully, S. Hume, J. J. Gardson, J. R. Harts, J. Hully, S. Hulls, J. Hully, J. Hull, J. H. Harts, J. Harts, J.
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PRI 04-FEB-2000

Euteleostomi;

Department of Genetics, Washington Park Avenue, St. Louis, Missouri 63108, USA

Washington Missouri 63108, USA

Department of Genetics, Park Avenue, St. Louis,

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Direct Submission
Submitted (04-FEB-2000) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center: Washington University Genome Sequencing Center
                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (Dases 1 to 171370)
Kalicki, J., Kellen, J. and O'Brien, D.
The sequence of H. saplens PAC clone RP1-186K10
                                                 AC004021 171370 bp DNA linear PRI
Human PAC clone RP1-186K10 from 5q31, complete sequence.
AC004021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
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University, 4444 Forest
3 (bases 1 to 171370)
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Waterston, R.
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Summary Statistics

Genome Center

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This clone was provided for sequencing by Dr. Michelle M. Le Beau in the Department of Medicine, University of Chicago, Chicago IL; and Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this clone, see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NEIGHBORING SEQUENCE INFORMATION:
The actual start of this clone is at base position 1 of RP1-186K10;
actual end is at 171370 of RP1-186K10. The orientation of this
NOTICE: This sequence may not represent the entire insert of this folone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                     This sequence was finished as follows unless otherwise noted: all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ρλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This clone was derived from human PAC library RPCI-1, prepared by Pieter de Jong and coworkers at Roswell Park Cancer Institute, using the method described by Ioannou et al., Nature Genetics 6:84-9 (1944). The library is from one male donor. For further details, see http://bacpac.med.buffalo.edu/
The clone is available from Genome Systems, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (http://www.genomesystems.com).
VECTOR: pCYPAC2
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Db 39182 TGAAAATACCATGACGAAAA 39163

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repeat\_region

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This clone contains STS AFM350ybl (NID:{\tt g1051891}) and EST53547 (NID:{\tt g1347444}).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /rpt_family="Retroviral"
9041. 10574
/note="CpG_island (%GC=73.7, o/e=0.70, #CpGs=115)"
10335. 10420
                                                                                                                                                                                                                                                                                           /rpt_family="L1"
1290_.2612
-.2612
2617..2679
/rpt_family="MER81"
3511..3643
3791..4239
                                 1. 171370
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
                                                                                                                                                                                                                                                                       /rpt_family="Retroviral"
5017. .5328
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/rpt_family="MER1_type"
18900. .18902
                    Location/Qualifiers
                                                                                         /clone="RP1-186K10"
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1. .1157
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4249. 4551
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4553. .4936
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10416. .10523
/rpt_family="Alu"
10535. .10594
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10732. .10988
/rpt_family="L1"
11023. .14892
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|/rpt_family="L1"
|15585. 15767
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20863. .22033
/rpt_family="L1"
22147. .24390
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18903. .18949
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19618. .19768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /rpt_family="L2"
18950. .18972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /rpt_family="L1"
19769. .20895
                                                                                /map="5q31
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                    FEATURES
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AC116356 175838 bp DNA linear HTG 10-APR-2002 HOMO sapiens chromosome 5 clone RP11-654L21, WORKING DRAFT SEQUENCE, 3 unordered pieces.
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100.0%; Pred. No.
                                                                                                        /rpt_family="Alu"
28460. .28510
/rpt_family="7SLRNA"
28548. .28834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /rpt_family="(TAA)n"
                                                                                                                                                          /rpt_family="Alu"
28855. 29167
/rpt_family="Alu"
29768. 30055
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/rpt_family="L1"
/rpt_family="Alu"
32124. 32489
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34315. 34609
/rpt_family="Alu"
7782. 34932
/rpt_family="L2"
34935. 35152
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/rpt_family="MIR"
36512, 3660
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38742. 38863
/rpt_family="MIR"
40308. 40599
7.rpt_family="Alu"
41127. 41200
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1356. .41728
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1917. .42152
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2647. 32732
/rpt_family="L1"
24614. .25397
/rpt_family="L1"
25396. .26577
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37957. .38046
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43252. .4354
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43535. .43594
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2468. .42623
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16882. .37126
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rpt_family≕"MIR"
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rpt_family="L2"
3613. .33706
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2169. .42459
                                                    rpt_family="L1"
7204. .27824
                                                                                rpt_family="L1"
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tive 0;
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Best Local Similarity
Matches 20; Conserv
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AC116356/C
LOCUS
DEFINITION
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L-2,4-diaminobutyrate decarboxylase ddC TR:Q9SOP8 (EMBL:AB032468) (490 aa) fasta scores: E(): 0, 39.3% id in 468 aa, and to Acinetobacter baumannii L-2,4-diaminobutyrate decarboxylase ddC SW:DDC_ACIBA (Q43908) (510 aa) fasta scores: E(): 0, 38.3% id in 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="putative ferric iron reductase"
/protein_id="CAC90351.1"
/db_xref="G1:15979571"
/db_xref="SPTREMBL:08ZF25"
/translation="WSNTAQUIPSFIGLIADITELFEKTFAHFSRTLKVNADDIPEE
TMSFHTWSSIDNFPTLIQKYRDEYYGDNDLKPNDKALYSLWSQWYFGLIIPPMMLLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EYPQTIDTHHKNFKVLFHHSGRPEVYYYQLKWQSQDFGTLLERYYLLLNHHVYPTAEK
IESYQGINGRLLWNNIGYLMFWYLGEFKGRLGDDLYQSIINGLFMELSLPNGQDNPLY
RTVMLRNGTLQRRSCCQRNKLPGVRSCHDCPLEKPPLNLIS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Similar to Escherichia coli ferric iron reductase
protein Fihr SW.FHUF_ECOLI (P39405) (262 aa) fasta scores:
E(): 8.4e-33, 35.0% id in 246 aa"
/codon_start=1
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ARIKAVFTLVDKPFSGVLPSELSPDFYCIDLNQPLTSLDSALDELQQLYIKDAIYFHH
                                                                                                                                                                                              Parkhill, J., Wren, B.W., Thomson, N.R., Titball, R.W., Holden, M.T.G., Parkhill, J., Wren, B.W., Thomson, N.R., Titball, R.W., Holden, M.T.G., Prentice, M.B., Sebalhia, M., James, K.D., Churcher, C., Mungall, K.L., Baker, S., Basham, D., Bentley, S.D., Brooks, K., Cerdeno-Tarraga, A.M., Chillingworth, T., Cronin, A., Davies, R.M., Davis, P., Dougan, G., Feltwell, T., Hamlin, N., Holroyd, S., Jagels, K., Leather, S., Karlyshev, A.V., Moule, S., Oyston, P.C.F., Quail, M., Rutherford, K., Slumonds, M., Skelton, J., Stevens, K., Whitehead, S. and Barrell, B.G. Nature, 413 (6855), 523-527 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Details of Y. pestis sequencing at the Sanger Centre are available on the World Wide Web.
                                                                                                                                                          Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (04-00T-2001) Submitted on behalf of the Yersinia sequencing team, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 ISA E-mail: parkhill@sanger.ac.uk
       Yersinia pestis strain CO92 complete genome; segment 9/20.
AJ414149 AL590842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (URL, http://www.sanger.ac.uk/Projects/Y_pestis/)
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/protein_id="CAC90352.1"
/db_xref="G1:15979572"
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1. .193050
/organism="Yersinia pestis"
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/gene="YPO1529"
1303. ?PF^
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/gene="YP01528"
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                                                      AJ414149.1 GI:15979570
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Parkhill, J.
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          DEFINITION
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AUTHORS
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                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (27-MAR-2002) Production Sequencing Facility, DOE Joint
Geomem Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (Dases 1 to 175838)
DOE Joint Genome Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (10-APR-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Apr 10, 2002 this sequence version replaced gi:19745038.
                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Consensus quality: 173992 bases at least Q40
Consensus quality: 174716 bases at least Q30
Consensus quality: 175005 bases at least Q30
Estimated insert size: 175000; agarose-fp estimation
Estimated insert size: 175030; sum-of-contigs estimation
Quality coverage: 5.82 in Q20 bases; sum-of-contigs estimation
Quality coverage: 5.79 in Q20 bases; sum-of-contigs estimation
* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="RPCI human BAC library 11"
36757 c 39091 g 52038 t 219 others
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AC116356.2 GI:20127977
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
Homo sapiens.
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Center Project Name: 1545925
Center clone name: RPCI-11_654L21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                   Sequencing of Human Chromosome 5
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site: http://www.jgi.doe.gov
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Center Code: JGI
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DOE Joint Genome Institute.
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DOE Joint Genome Institute.
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Matches 20; Conservative
                                                                             Homo sapiens
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Homo sapiens
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/product.mutative siderophore biosynthetic enzyme"
/protein_id="CAC90153.1"
/db_xref="GI:15979573"
/db_xref="GI:15979573"
/db_xref="GI:15979573"
/db_xref="SPTREMBL.GBZF23"
/translation="MRPYDFIGIGIGPFNLGLACLTQPLNDVCCLFIDOKAGFDWHPG
MMLGSATGPFREMSDLYTLASPTHEJSFLWIYTRQOGSTHEFLCKKLVLGTGPSPHI
PECCQPFIQOIVMSGQYLEHKVALOKKRAITILGSGGSAAEIFYDLLCEIDRFDYQLN
WLTRSPRELPLEYTKLILEMTSPEVDYFYHLPPEKRDELNLTHKPLYKGINGTLND
IFDLLYTKLINGALNVNLYTNSELQKVSSHDGKGLHLSVLQHEQNQLFTLETEGAVL
AGGYHYQPPFIEGIRGITHWDNKGRYEVORNYSIDBNNTIFVONVELHTHGFVTPDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note-"Similar to Bordetella bronchiseptica alcaligin
blosynthesis enzyme SW:ALCA_BORBR (044740) (461 aa) fasta
scores: E(): 0, 49.6% id in 425 aa, and to Streptomyces
coelicolor putative monocygenase Scc105.14 TR:09L071
(EMBL:AL163641) (413 aa) fasta scores: E(): 0, 53.7% id in
                                                  QKAAALLGLGYNAVVAVPYDSEFKMDAQALDOSIALCLSQGNIPLAIVATTGTTDFGS
IDPHHTISTLAKOYGLMLHYDAAVGGLLVSSHYEQLLSGTEMADSYTVDYHKSFFQP
VSCSAFFYKDKQHFSYLTYHEYLNPLSASLEGFPNLVNKSIQTTRREDALKLMLTLR
IMGAKQLGLAFEHYMDTAQQAYQLMLPNPYFELIHRPVLSTLYFRFWEQPRSDDDID
RTNAYIRKALFREGHTVIAGTKVNGKQYLKFTFLNPTTTLQHLNEIVDAIITEGKNYP
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/product="putative siderophore biosynthetic enzyme"
/product="putative siderophore biosynthetic enzyme"
/protein_id="CAC90354.1"
/db_xref="c1:19579574"
/db_xref="SPTREMBL:082F22"
/translation="MNNAERNIESDBTVVRSGGFQLRPLVLAHDVTWLTDWVNREYAHY
WGMGGYSPQQVKAFYGELWTSQPGGVFVGVTQQQPAFLLERYLAQHDVTADTYPAQPD
DVGMHILVAPPVERTTGFTWRFPQALWTFIESDPTVARIVVEPDVRNEKIHKLNKRAG
FYYQQQLTLEHKTAMLAFCTREQYRLALQKEHQ"
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PKYVAHLNCPVVLPAVLAESIISTLNSSLDTWDQSAGATLIEQKVLDWTRDKMALGSQ
GDGIFTSGGTQSNLMAILLARDHFCHQRDANHQNKLQGLPADSHKFRIFTSVVSHFST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Similar to Bordetella bronchiseptica AlcB alcB 7.78.78.id in 174 aa, and to Streptomyces coelicolor putative acetyLtranferase scc105.15 TR:09L070 (EMBL:AL163641) (184 aa) fasta scores: E(): 3e-23, 39.5%
                                                                                                                                                                                                                                /note="pfam match to entry PP00282 pyridoxal_deC, Pyridoxal-dependent decarboxylase conserved domain, score 165.20, E-value 2.7e-47"
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/gene="YPO1530"
/note="PS00013 Prokaryotic membrane lipoprotein lipid
attachment site."
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/transl_table=11
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/gene="YPO1531"
/note="alcB"
                                                                                                                                                                                                                             1699. .2619
/gene="YPO1529"
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/gene="YPO1530"
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/gene="YPO1530"
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/gene="YPO1531"
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/gene="YPO1532"
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/gene="YPO1532"
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/translation="mRSQRELTSPWTPLENPGDISDKPRLTTQKLSLGYGQQLIINKL
SLSIKNGAFSVIIGPNGCGKSTLLRALSRSLLPQNGSIRLDQQDIQHYKAKVFARQLS
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ELSGGQRQRAWFAWTLAQHTPIVLLDEPTTYLDIAHQIEMLDLCQELQQQGKTLVLVL
HDINQALRYATHLIMLKEGQIYAEGLPESIVTEDSIAAVFGLRCRIITDPESGKPLVI
                                                                                                                                                                                                                           /translation="MMMDLSAPLSPHQSLELPHLQPVLWQKVNRLHLCKAISEFSHEC
LIAPQRWIDPEDSGYDYYQUVAAAADKPANYYFRARRALALDHWLIDPDSLHKYVNBK
SIDLDLLLFIIEFKRQLSISERVLPYYLEETISTLXSSAFKHCRTGISATALVNASFQ
IIEKEMMEGHPSFVANNGRIGFDAQDFORFSPBAASDVHLVWLAAHKSKAHFACTEQL
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ATP-binding component"
//protein_id="CAC90356_1"
/db_xref="G1:15979576"
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                                      /product="putative siderophore biosynthetic enzyme"
protein_id="CAC9035:1"
/db_xref="GI:15979575"
/db_xref="SPTREMBL:082F21"
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Human DNA sequence from clone RP5-1087E8 on chromosome
1442.11-42.2, complete sequence.
AL353689.26 GI:16304807
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/gene="YPO1533"
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/gene="YPO1533"
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.00.0%; Pred. No.
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/transl_table=11
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Noore, M.

Direct Submission

Lineat Submitted (19-ocr-2001) Sanger Centre, Hinxton, Cambridgeshire,

CBIO 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk

on oct 21, 2001 this sequence version replaced gi:15983876.

During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality)=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one Mi3 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em; EMBL; Sw;
SWISSPROT; Tr:, TREMBL; Wp; WORNPEP; Information on the WORMPEP
database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping
froup.
Further information can be found at
http://www.sanger.ac.uk/RGP/Chr.
RP5-1087EB is from the library RPCI-5
constructed by the WORNPEP
http://www.sanger.ac.uk/RGP/Chr.
RP5-1087EB is from the library RPCI-5
constructed by the group of
Pleter de Jong. For further details see
htttp://www.chorn.org/Dacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence is the entire insert of clone RP5-1087E8 The true left end of clone RP11-1B20 is at 155425 in this sequence. The true right end of clone RP11-375H24 is at 75234 in this sequence. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note-"Tandem repeat. Forced join. Gap size estimated to
be approximately 600bps by restriction digest data."
38361
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 195829)
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/note="Sequence from overlapping clone RP11-375H24
(AL391628). Assembly confirmed by restriction digest."
39840. .39867
/note="Single clone region. Assembly confirmed by restriction digest data."
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/clone_lib="RPCI-5"
13995. .14136
/note="Sequence from overlapping clone RPII-375H24
/AL391628).Assembly confirmed by restriction digest."
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3.0%; Score 20; DB 9; Length 195829;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 20; Conservative 0; Mismatches 0; Indels 0
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
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AUTHORS
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Search completed: January 21, 2003, 00:05:22 Job time : 3147 secs

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Gaps

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January 20, 2003, 23:02:09; Search time 230 Seconds (without alignments) 6550.378 Million cell updates/sec
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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length: 2000000000
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Title:

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Post-processing: Listing first 1000 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

### M. capsulatus gene M. capsulatus gene DNA encoding novel Description ABQ91613 ABQ91612 AAS85924 Ω 23 24 24 Query Match Length DB 1881 522 603 Score 202 Result è. O

## ALIGNMENTS

RESULT

The invention relates to isolated polymetractice (1) and to polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The and gene mapping, and in recombinant production of (II). The polymerlead expressed genes (1) is useful in gene therapy techniques for identifying expressed genes. (1) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical inaging of sites expressing (II). (I) are useful for treating clisorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in casponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and diagnostic coding sequences of fite invention.

Camino acid sequences. Abs64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this partent did not appear in the printed specification, but was obtained in electronic format directly from WIPO ö Gaps Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss. New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess ö Score 23; DB 23; Length 1881; Pred. No. 0.074; 0; Mismatches 0; Indels ( The invention relates to isolated polynucleotide (I) and Sequence 1881 BP; 419 A; 469 C; 533 G; 460 T; 0 other; ONA encoding novel human diagnostic protein #21728. at ftp.wipo.int/pub/published\_pct\_sequences 100.0%; Prec. ... Claim 1; SEQ ID No 21728; 103pp; English. 133 CTGTTCAATAAACCCTACGATGT 155 591 CTGTTCAATAAACCCTACGATGT 569 BP. RESULT 2 ABQ91613 ID ABQ91613 standard; DNA; 522 3.48; 23; Conservative Local Similarity Query Match Matches Best ŏ g

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Search completed: January 20, 2003, 23:12:43 Job time: 231 secs
14-JAN-2002; 2002WO-NO00019.
                                                                                                                                                                                                                         Lillehaug JR,
                                                                                                                                                                                             Birkeland NK,
                                                                                                                                                                                                                                             Salzberg SL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a novel DNA array giving a representation of a number of Methylococcus capsulatus genes. The method of the invention is useful for determination of the differential expression of the genes of M. capsulatus, and for Studying gene expression on a genomic scale and in gene expression and in seayes of M. capsulatus genes. The sequences shown in ABQ90016-ABQ91855 represent M. capsulatus genes for use in arrays of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel DNA array useful for determining differential expression of Methylococcus capsulatus genes, comprises polynucleotides or oligonucleotides representative for a selective number of Methylococcus capsulatus genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                  Micro array; gene; ds; differential expression; gene expression.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , Jonassen I, Jensen HB, Lien T
Eisen JA, Fraser CM, Durkin AS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.0%; Score 20; DB 24; Length 522; 100.0%; Pred. No. 2.9; tive 0; Mismatches 0; Indels
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                                                                                                                     M. capsulatus gene #1598 for DNA array.
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Lillehaug JR, Lossius I, E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABQ91612/c
ID ABQ91612 standard; DNA; 603
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12-JAN-2001; 2001NO-0000239
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                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                      ABQ91613;
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                                                                                                                                                                                                                                                                                                                                                                                                                Methylococcus capsulatus genes, comprises polynucleotides or oligonucleotides representative for a selective number of Methylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                Novel DNA array useful for determining differential expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ó;
                                                                                                                                                                                            Lien T;
                                                                                                                                                                                            Jensen HB, Lien T
ser CM, Durkin AS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3.0%; Score 20; DB 24; Length 603; 100.0%; Pred. No. 2.9; or Indels rative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 603 BP; 135 A; 169 C; 180 G; 119 T; 0 other;
                                                                                                                                                                                         , Jonassen I, Jensen
Eisen JA, Fraser CM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 14; Page 608-609; 678pp; English.
                                                                              (UNIF-) UNIFOB STIFTELSEN UNIV BERGEN. (TIGR-) TIGR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              245 GCGACAGCGAGGGGCTGCTG 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               233 GCGACAGCGAGGGGCTGCTG 214
12-JAN-2001; 2001NO-0000235
12-JAN-2001; 2001NO-0000239
                                                                                                                                                                                            Eidhammer I,
                                                                                                                                                                                                                                Lossius I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                        WPI; 2002-557818/59.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 capsulatus genes
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
```

OM nucleic - nucleic search, using sw model

January 20, 2003, 23:07:39 ; Search time 50 Seconds (without alignments) 4103.335 Million cell updates/sec Run on:

US-09-252-691C-1394 669 1 gctataatgcggcaattgat......ttacccctaaggagaactga 669 Title: Perfect score: Sequence:

OLIGO\_NUC Gapop 60.0 , Gapext 60.0 Scoring table:

441362 seqs, 153338381 residues Searched:

20 Word size :

0 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database :

Issued\_Patents\_NA:\*
1: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq:\*
2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq:\*
3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq:\*
4: /cgn2\_6/ptodata/2/ina/PCTUS\_COMB.seq:\*
5: /cgn2\_6/ptodata/2/ina/PcTUS\_COMB.seq:\*
5: /cgn2\_6/ptodata/2/ina/PcTUS\_COMB.seq:\*
6: /cgn2\_6/ptodata/2/ina/PcTUS\_COMB.seq:\*
6: /cgn2\_6/ptodata/2/ina/PcTUS\_COMB.seq:\*
6: /cgn2\_6/ptodata/2/ina/PcTUS\_COMB.seq:\*
7: /cgn2\_6/ptodata/2/ina/PackfilesI.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description Ω % Query Score Match Length DB

No matches found

٠ 9 Result

Search completed: January 21, 2003, 00:30:41 Job time : 50 secs

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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM nucleic - nucleic search, using sw model
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January 20, 2003, 23:01:24 ; Search time 56 Seconds (without alignments) 5326.534 Million cell updates/sec

US-09-252-691C-1394 669

Title: Perfect score:

Run on:

Sequence:

1 gctataatgcggcaattgat......ttacccctaaggagaactga 669 OLIGO\_NUC Gapop 60.0 , Gapext 60.0 Scoring table:

393868 seqs, 222934149 residues Searched:

20 Word size :

0 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database

Published\_Applications\_NA:\*

1: / cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*
2: / cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*
3: / cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*
3: / cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*
4: / cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*
5: / cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*
7: / cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*
3: / cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*
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4: / cgn2\_6/ptodata/2/pubpna/US00\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description Query Score Match Length DB No. Result

No matches found

Search completed: January 20, 2003, 23:08:37 Job time : 56 secs

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BI249598 602996256

13 BI249598

1075

3.0

20

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A2296025 RPCI-23-6
BE115864 UI-R-BSI-
AV523923 AV523923
BH160291 ENTSEOUTR
BH570517 BOHIJ41TR
AL421622 T3 end of
                                                                                           (without alignments)
5530.771 Million cell updates/sec
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                                                                                                                                                            1 gctataatgcggcaattgat.......ttacccctaaggagaactga 669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Description
                                                                            January 20, 2003, 23:07:04; Search time 1959 Seconds
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                      ^
                                                                                                                                                                                                                                16154066 segs, 8097743376 residues
                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                          Post-processing: Listing first 1000 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
                                                  - nucleic search, using sw model
                                                                                                                                                                                         OLIGO_NUC
Gapop 60.0 , Gapext 60.0
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669
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em_gss_pro:*
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Maximum DB seq length: 2000000000
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em_gss_hum:*
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em_gss_fun:*
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gb_est2:*
gb_htc:*
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A2296025 BE115864

AV523923 BH160291 BH570517 CNS06YXS

17 10 10 17 17

497 522 565 699 818 964

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497 bp DNA linear GSS 27-JUL-2000
RPCI-23-62013.TJB RPCI-23 Mus musculus genomic clone RPCI-23-62013,
AZ296025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCUS BE115864 522 bp mRNA linear EST 13-JUN-2000 DEFINITION UI-R-BS1-axx-c-03-0-UI.s1 UI-R-BS1 Rattus norvegicus cDNA clone
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                                                                                                                                                                                                                                                                                                                                       Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret, B., Levins, M., Mcgann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P. and Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: Szhaoétigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Library availability, please contact Pieter de Jong
(pieterédejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 62 row: 0 column: 13
Seg primer: SP6
Class: BAC ends.
                                                                                                                                                                                                                                                           Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 497)
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0
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Pred. No. 0.31;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                       Mouse BAC End Sequences from Library RPCI-23 Unpublished (1999)
Unpublished (1999)
Unpublished (1999)
Unpublished (1999)
Unpublished (1999)
Cohter_GSSS: RRCI-23-62013.TVB
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
7712 Medical Center Dr., Rockville, MD 20850, USA
7712 Medical Center Dr., Rockville, MD 19850, USA
Fax: 301 838 0200
ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. .497 /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:10090"
/clone="RPCI-23-62013"
/clone_lib="RPCI-23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /strain="C57BL/6J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex="Female"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 3.3%; Sc
Best Local Similarity 100.0%; P
Matches 22; Conservative 0;
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                                                                                                                                                                                          AZ296025.1 GI:9537810
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                                                                                                                                                                                                                                       house mouse
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BE115864/c
                                                                                                                        DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
JOURNAL
                                                                                                                                                                                                                                                             ORGANISM
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                                                                                                                                                                      ACCESSION
                                                                                                                                                                                          VERSION
KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                               AUTHORS
                                                            RESULT 1
AZ296025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURES
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125 c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
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LOCUS
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AUTHORS
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TITLE
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /strain="Sprague-Dawley"
/db_ref="texton:10116"
/clone="U1-R-BS1-axx-c-03-0-UI"
/clone_lb="U1-R-BS1-axx-c-03-0-UI"
/clone_lb="U1-R-BS1-axx-c-03-0-UI"
/dev_stage="embryonic 13 dpc"
/lab_host="Whil0B (Life Technologies)"
/note="Vector: pT7730-Pac (Pharmacia) with a modified
polylinker; Site_1: Not 1; Site_2: Eco RI; The UI-R-BS1
library is derived from 13 dpc whole embryo tissue. For a
detailed description of the library from which this clone
was derived, please visit our web site at
ratest.eng.ulowa.edu.
TAG_IIB-UI-R-BS1
TAG_ISSUB=embryo at 13 dpc
TAG_SEQ-AATCC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ó
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                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence contained an oligo-dT track that was present in the oligonuclectide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the CDNA between the NoIs stend the oligo-dT track served to verify it as a clone from the normalized embryo at 13 dpc library CDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Seq primer: M13 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             thale cress.
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AV523923 Arabidopsis thallana aboveground organs two to six week old Arabidopsis thallana cDNA clone APZL44a05F 3', mRNA sequence.
                                                                                                                                                                                             Bonaldo, M.F., Lennon, G. and Soares, M.B. Normallzation and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                    University of Iowa 451 Ecsearch Building Iowa City, IA 52242, USA Tel: 319 335 8250 Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                               Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
UI-R-BS1-axx-c-03-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                               Email: msoares@blue.weeg.uiowa.edu
                                                                                                                                                                                                                                                          Genome Res. 6 (9), 791-806 (1996)
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BE115864.1 GI:8508009
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nes 20; Conservative
                                                                               Norway rat.
Rattus norv
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TITLE
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Matches
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AV523923
LOCUS
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KEYWORDS
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 565)
Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries
DNA Res. 7, 175-180 (2000)
                                                                                                                                                                                                                                                                                       The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENTSEO1TR Entamoeba histolytica Sheared DNA Entamoeba histolytica genomic, DNA sequence.
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Contact: Brendan J Loftus
Contact: Brendan J Loftus
Contact: Brendan J Loftus
Contact: Brendan J Loftus
The Institute for Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Fax: 301 838 0208
Fax: 301 838 3543
Email: bjloftus@tigr.org
Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
DNA library
Seq primer: M13-Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      six-week old"
/tissue_type="aboveground organs"
/dev_stage="two to six-week old"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="APZL44a05F"
/clone_lib="Arabidopsis thaliana aboveground organs two
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Entamoeba histolytica
Eukaryota; Entamoebidae; Entamoeba.
1 (bases 1 to 699)
Loftus, B., Wang, Z., Van Aken, S. and Fraser, C.
Determination of clone end sequences from Entamoeba histolytica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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/db_xref="taxon:5759"
/clone_lib="Entamoeba histolytica Sheared DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.0%; Score 20; DB 10; Length 565; 100.0%; Pred. No. 4.8; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Arabidopsis thaliana"
/strain="Columbia"
/db_xref="taxon:3702"
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High quality sequence stop: 264.
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                                                                                                                                                                                                                                                                Contact: Erika Asamizu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    543 CATTCGCTACGCCATGGGCA 562
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Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: sequefégenoscope.cns.fr) This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces hansenii var. hansenii, Pichia sorbitophila, angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.

Location/Qualifiers
                                                   CNSO6XXS 964 bp DNA linear GSS 06-JUL-2001 T3 end of clone AY0AA014A03 of library AY0AA from strain CBS 6340 of Kluyveromyces thermotolerans, genomic survey sequence.
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/note="similar to Saccharomyces cerevisiae ORF YDR022c [
CIS1 ; involved in suppression of CIK1 mutation ]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 964)
Malportuy,A., Llorente,B., Blandin,G., Artiguenave,F., Wincker,P.
and Dujon,B.
                                                                                                                                                                                                                                                                                                                                                                Bolotin Fukuhara, M., Bon, E., Brottier, P., Casaregola, S., Belotin Fukuhara, M., Bon, E., Brottier, P., Casaregola, S., Belotin Fukuhara, M., Dujon, B., Durrens, P., Lepingle, A., Llorente, B., Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S., Saurin, W., Tekala, F., Toffano Nioche, C., Wesolowski-Louvel, M., Wincker, P. and Weissenbach, J. Toffano Nioche, C., Wesolowski-Louvel, M., Wincker, P. and Weissenbach, J. Toffano Store February Species for molecular evolution studies

FEBS Lett. 487 (1), 3-12 (2000)
                                                                                                                                                                                                                                          Kluyveromyces thermotolerans
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
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                                                                                                                                                                                                                                                                                          Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
1 (bases 1 to 964)
Souciet, J.L., Aigle, M., Artiguenave, F., Blandin, G.,
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/note="putative V (GTA) tRNA gene"
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240 c 234 g 222
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FEBS Lett. 487 (1), 61-65 (2000)
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/clone="AYOAA014A03"
/clone_lib="AYOAA"
/note="end : T3"
                                                                                                                                                                                                               Kluyveromyces thermotolerans.
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AL421622.1 GI:12204820
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        RESULT 6
CNSO6YXS
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/note-"Vector: pHOS1; Site_1: Bst I; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark and Diamond (Clark, C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a method for isolate identification. Exp. Parasitol. 77.450.). The DNA was mechanically sheared to give a tight size distribution (-2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University Press, 1999)."
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BOHIJ41TR BOHI Brassica oleracea genomic clone BOHIJ41, DNA
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 818)
Town,C.D., van Aken,S., Utterback,T. and Fraser,C.M.
Whole genome shorty sequencing of Brassica oleracea
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/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOS1 using BstXI linkers"
127 c 111 g 304 t
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DNA is from a doubled haploid provided by Tom Osborn.
Geg primer: TR
Class: sheared ends.
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/strain="TO1000bH3"
/db_xref="taxon:3712"
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Contact: Chris Town
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NIH-MGC http://mgc.nci.nih.gov/.

NITIONAL Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys CDNA Library Preparation: Life Technologies, Inc.

CONA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CONA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

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